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cortex"
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ra, A., Itoh, M., Kawai, J., Shibata, K.
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Pred. No. 4.1e-146;
0; Mismatches 15;
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  Shinagawa, A., Saito,
Fukuda, S., Hara, A.,
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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AL Unpublished (2001)

On Jul 7, 2000 this sequence version replaced gi:8960678.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research (RUKEN)

On Jul 7, 2000 this sequence version replaced gi:8960678.

Laboratory for Genome Exploration Research (RUKEN)

1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922

Fax: 81-4
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                                                                                                                                            tissue type="cortex"
dev_stage="10 days neonate"
lab_host="DH108"
                                                                                           organism="Mus musculus"
                                                                                                      'mol_type="mRNA"
|db_xref="taxon:10090"
|clone="A830014H23"
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/clone lib="NIH MGC 256"
/clone lib="Organ: Occyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; cDNA was primed using oligo-dT primer:
Site_2: Not1; cDNA was primed using oligo-dT primer:
5: pGACTAGATCGGAGGGGCGCC(T): 25-3 and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC 257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
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musculus cDNA clone
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AACGCCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAA
                                                                                                     CGTTTCTGCTAGATGGGCTTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCT
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Capbs-rémail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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High quality sequence stop: 601.
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AGENCOURT 30259223 NIH MGC 256 Mus
IMAGE:30935466 5', mRNA sequence.
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/db_xref="taxon:10090"
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/clone_lib="NIA Mouse 15K cDNA Clone Set"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a latercoyet, embryonic part of 127.5 clone is among and 127.5 clone is among and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with oligo(dT)-Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, proc. Natl. Acad. Sci. U S A, 97: 9127-9112; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse develolpment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from
                                                                                                                                                                                                                           595 bp mRNA linear EST 18-DEC-2003
H3102B03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
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  CCICTTCCCTTTCCAAATTCTTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAA 1242
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 595)
                           76 CCTCTTCCCAAATTCTTCAGACAGAG-TACTTGGATATAAAGCCTGTGAA 18
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dev_stage="Clones arrayed from a variety of cDNA
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
Visit http://lgsun.grc.nia.nih.gov/cDNA/15K.html for details.
Plate: H19D:/ Tow: B column: 03
Seg primer: -21NA1 Reverse
High quality sequence stop: 595
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Other_ESTs: H3102B03-3
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/organism="Mus musculus"
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db xref="missEr:H3102B03-5"
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/clone="H3102B03"
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TITLE

FEATURES

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Mus musculus (house mouse)

EST.

Mus musculus

ENkaryoria, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

EUKaryoria, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 731)

RIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

CDNA Library Preparation: Express Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 991 TGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTG 1050
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IMAGE:30936113 5', mRNA sequence.
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extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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                                                                                                                                                                                                                                                  511 CCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAAGCGGTC
                                                                                                                                                                                                                                                                                                      GAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGAC
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                              1;
                                                                                                                                    Length 595;
                                                                                                                                                                                           Indels
                                                                                                                                       DB 4;
                                                                                                                                       Score 582.4; DB 4;
Pred. No. 2.6e-131;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO809618
CO809618.1 GI:51027468
                                                                                                                                    Query Match
Best Local Similarity 99.7%;
Matches 594; Conservative
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
UI-M-BH3-awu-b-08-0-UI.rl NIH BWAP M.S4 Mus musculus CDNA clone
UI-M-BH3-awu-b-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
7101: 301 443 196
Fax: 301 443 8890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: M13 Reverse
                                                                           BF471866
BF471866.1 GI:11541049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 99.5
3; Conservative
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Best Local Si
Matches 593
                                                                                                                                       EST
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                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
PUBMED
                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                               /clone="Image: 3093613"
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/lab_host="DH10B TonA"
/lab_host="DH10B TonA"
/lab_host="DH10B TonA"
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Site_2: Not1; cDNA was primed using oligo-dT primer:
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5: pGACTAGATCTGAGATCGGAGGCGCCC(7)25-3, and cloned into
bright an average insert size of 1.2 kb. This is a
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC 257)
pand was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGTTGC
                                                                                    þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1191 row: e column: 18
High quality sequence stop: 605.

1. 731
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 571.4; DB 7;
Pred. No. 1.3e-128;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.8%;
Matches 572; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
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BF471866/c
LOCUS
                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                   FEATURES
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/gtrain="C57BL/6J"
//db xrefe".taxon:10090"
//db xrefe".taxon:10090"
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//lone lib="WiH BMAP M S3"
//clone lib="Wih BMAP M S3"
//converted to double-stranded circles and electroporated converted to double-stranded circles subtracted lib="Wih BMAP M S4"
//converted to double-stranded circles and electroporated converted to double-stranded circles and electroporated converted to double-stranded circles subtracted lib="Wih BMAP M S4"
//converted to double-stranded circles subtracted lib="Wih BMAP M S4"
//converted to double-stranded circles subtracted lib="Wih BMAP M S4"
//converted to double-stranded circles subtracted lib="Wih BMAP M S4"
//converted to double-stranded circles subtracted lib="Wih"
//converted to double-stranded circles subtracted to double-stranded circles subtracted to double-stranded circles subtracted lib="Wih"
//converted to double-stranded circles denome Research
//converted to double-stranded circles denome Research
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CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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99.5%; Pred. No. 2.2e-128;
iive 0; Mismatches 1;
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/clone_lib="NIH MGC_256"
/note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;
Site 2: Not1; cDNA was primed using oligo-dT primer:
5'-pGACTACTACACGCGAGCGCCCCC(T)25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC 257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
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AGENCOURT 30246265 NIH MGC 257 Mus musculus cDNA clone
IMAGE:30935142 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGCACGCTGCAGCCTGCAGGGTGTCGAGCCAGCCCGACGCCCGATCGGGTTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACCCCGTGGCCACGCCCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACCCACGAAGGGAGAGNNGGAGCCCGCCATCCTCGGGGAACCGGAACCNNGAGC---GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                         40.9%; Score 522.8; DB 7;
.larity 91.8%; Pred. No. 1e-116;
Conservative 0; Mismatches 47;
                         /db_xref="taxon:10090"
/clone="IMAGE:30939000"
/lab_host="DH10B TonA"
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

LUpublished (1999)
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Tissue Procurement Dr. Kathleen Horner, Stanford University
CDNA Library Preparation: Express Genomics
cDNA Library Preparation: Express Genomics
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1198 row: column: 01
High quality sequence stop: 495.

Location/Qualifiers

Norea
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

PEATURES

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Unpublished (2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
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Laboratory for Genome Exploration
Sciences Center(GSC), Yokohama Institute
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Emnil: genome-rese@ger.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Muramatsu, M. and Hayashizaki, Y.
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., Chara, E.,
wagi, K., Fujiwake, S., Inoue, K., Togawa, K., Tawa, M., Ohara, E.,
watchiki, M., Yoneda, Y., Ishikawa, T., Cawa, M., Inoue, Y., Kira, A.
and Hayashizaki, Y., Maramatsu, M., Inoue, Y., Kira, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaruyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaruyota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
3 Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayateu,N., Hiramoto, K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Kouno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Sasaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,Y., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sasaki,D., Sato,K., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Togawa,A., Takahashi,F., Takaku-Akahira,S.,
Muramateu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN, integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Komno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                      BB704019 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420459B08 3', mRNA sequence.
531
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/lab_host="DH10B"
/clom_ost="ERH10B"
fertilīzed eggs"
                                                                                         tissue_type="in vitro fertilized eggs"
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/clone="7420459B08"
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/strain="C57BL/6J"
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/organism="Mus musculus"
/mol type="mkNA"
/mol type="mkNA"
/db xrefe"taxon:10090"
/db xrefe"taxon:10090"
/clone="IMAGE:30935142"
/lab host="MH MGC_257"
/note="Organ: oocyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not!; cDNA was primed using oligo-dr primer:
5: pGACTAGTTCTAGATCGCAGCGCCCC(7125-3' and cloned into
the EcoRV/Not! sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
normalized library (primary library is NIH MGC_256) and
was constructed by Express Genomics (Prederick, MD). Note:
this is a NIH_MGC library"
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 546)
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                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Bmail: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                 Library Proparation: Express Genomics CDNA Library Proparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAMI188 row: m column: 07
High quality sequence stop: 519.
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ilarity 98.5%; Pred. No. 9.2e-112;
Conservative 0; Mismatches 6;
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Best Local Simi
Matches 525;
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/lab_host="DHIOB TonA"
/clone_lib="NIH MGC_256"
/clone_lib="NIH MGC_256"
/clone_location oocyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1: CDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCCGCCC(T) 25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC_257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
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                                                         Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloA07 Bethesda, MD 20892
Email: Gapbs-r@mail.nih.gov
Tissue Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga-llnl.gov
Plate: NDAM1200 row: j column: 15
High quality sequence stop: 418.
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            of Health, Mammalian Gene Collection (MGC)
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93.5%; Pred. No. 2.3e-106;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30939686"
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                                            Unpublished (1999)
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Best Local Similarity 93.5
Matches 517; Conservative
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Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Dases 1 to 687)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGGATGCCCCTCGAGACCACCCCCCCCCAAAGCACGAGCAGCAGAGCGCCT
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
701-91. 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the ODNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized basal gangia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Botty-vere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / db xref="Losubou"
/ db xref="taxon:10000"
/ clone="UI-M-BH0-akc-d-12-0-UI"
/ dev stage="27-32 days"
/ lab host="DH10B (Life Technologies)"
/ lab host="DH10B (Life Technologies)"
/ clone lib="NIH BMAP M SI"
/ clone lib="NIH BMAP M SI"
/ lone="Vector: pT773D-pg; Site 2: Eco RI; The polylinker; Site 1: Not I; Site 2: Eco RI; The polylinker; Site 1: Not I; Site 2: Eco RI; The man liberary is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain.
TAG IISSUE-basal-ganglia
TAG LIB=NIH BMAP M SI
TAG EEQ=TGTAC"
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UI-M-BHO-akc-d-12-0-UI.s1 NIH BMAP_M_S1 Mus musculus cDNA clone
UI-M-BHO-akc-d-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ( Dases I to 499)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Pred. No. 8.9e-105;
); Mismatches 2;
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/mol_type="mRNA"
/strain="C57BL/6J"
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97044477
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99.2%;
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Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Merazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmanlai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 491)
S. Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishli,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koudak,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,P., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci.P., Shibata,Y., Hayatau,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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GAGCAGGACAAGGACCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTGTCAC
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/organism="Mus musculus"
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prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAAAGCACGGAGCAGACAAGGAGCCCCTGCGTTTCCAGTTCTTATAGCAGAAGTACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dav_stage="egg"
/lab_host="DH10B"
/clone lib="EKEN full-length enriched, in vitro
fertilīzed eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="in vitro fertilized eggs"
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98.2%; Pred. No. 1.4e-98;
iive 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="7420449J15"
                                                                                                                                                                                                                                                                                                                                        e mouse tissues.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="female"
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Best Local S
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                               477
299 GGACAAACGCCTGTCCTGCGACAGCTTCAGCTTCAAATACATCATTTAGTGAGAGTC 358
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB704648 BIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420466L07 3', mRNA sequence.
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                                                                                                                                                                                                                                Length 491;
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                                                                                                                                                                                                                               32.4%; Score 413.8; DB 2;
llarity 93.0%; Pred. No. 4.1e-90;
Conservative 0; Mismatches 32;
          'db_xref="taxon:10090"
'clone="7420466L07"
                            sex="female"
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AU044294 Mouse sixteen-cell-embryo cDNA Mus musculus cDNA clone J0917G09 3', mRNA sequence.

AU044294/c LOCUS DEFINITION

RESULT 15

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Systematic analyses of genes expressed in 16-cell mouse embryo (The ERATO/Doi Project at Wayne State University)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1002
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                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGATTTCGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                        Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 436;
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="00917G09"
/dev_stage="sixteen-cell-embryo"
/clone_lib="Mouse sixteen-cell-embryo cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 405.8; DB 1;
Pred. No. 3.6e-88;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                            Mus musculus (house mouse)
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llarity 97.0%;
Conservative 0
              GI:3979844
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Job time : 4411 secs
                                                                   Mus musculus
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            AU044294.1
EST.
AU044294
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                                                                                                                 REFERENCE
                                                                                                                                 AUTHORS
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Danio rer Zebrafish

Homo i Ношо

us-09-830-810a-1.rge

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Run on:

Sequence:

Searched:

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AF429315 Homo sapi
AL684264 Penicilli
AC048354 Homo sapi
AC149759 Bos tauru
AC1449759 Bos tauru
AC116408 Mus muscu
AC116408 Mus muscu
AC11580 Mus muscu
AC11580 Mus muscu
AC11024 Rattus no
AC11024 Rattus no
AC141024 Rattus no
AC141024 Rattus no
AC185393 Sequence
AC052857 Rattus no
AC18627 Nus muscu
AC18627 Nus muscu
AC18627 Nus muscu
CR407549 Danio rer
BX470223 Zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zygote arrest 1 (Zarl) is a novel maternal-effect gene critical for the occyte-to-embryo transition
Nat. Genet. 33 (2), 187-191 (2003)
22447938
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Mus musculus zygote arrest 1 (Zarl) mRNA, complete cds.
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Wu,X., Wang,P. and Matzuk,M.M.
Wu,X., Wang,P. and Matzuk,M.M.
Direct Submission
Direct Submission
Submitted (04-DEC-2002) Pathology, Baylor College of Medicine, One
Baylor Placa, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 1260) Wu,X., Viveiros,M.M., Eppig,J.J., Bai,Y., Fitzpatrick,S.L. and Matzuk,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ZAR1; maternal factor; contains atypical C8 PHD motif at C-terminus"
BX531269 C
BX571888 I
BX537133 A
AJ335296 I
AF429315 I
AC123764 I
AF429315 I
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AC137771
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Mus musculus
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AY19389 Mus muscu
AC122733 Mus muscu
AL671880 Mouse DNA
AC107686 Mus muscu
AC125519 Rattus no
AC12593 Rattus no
AC126848 Mus muscu
AY191416 Homo sapi
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Takifugu
Danio rer
                                                                   January 5, 2005, 14:55:31; Search time 5526 Seconds (without alignments) 10928.148 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                 GGGCTAATGGAATGGACAAGTGAGCTTTCCCCCTCTTCACCTCTTCCCTTTCCAAATTC
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             TCAAACAGTTCTGCCGAGTGTGTGGGAAATCCTACAACCCTTACAGAGTGGAGGACATCA
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                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1280)
Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M.
Zygote arrest 1 (zarl) is an evolutionarily conserved gene
expressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                                                                                                                                                                                                                                                                                                                         mRNA linear ROD
1 (Zarl) mRNA, complete
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Wu,X. and Matzuk,M.M.
Direct Submission
Submitted (24-APR-2003) Pathology, Ba
Baylor plaza, Houston, TX 77030, USA
Location/Qualifiers
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Rattus norvegicus zygote arrest
AY283175
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Pred. No. 2.1e-248;
0; Mismatches 1; Indels 1;
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Мив musculus zygote arrest 1 (Zarl) gene, complete cds.
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the oocyte-to-embryo transition
Nat. Genet. 33 (2), 187-191 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-JAN-2003) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Sequence update by submitter
On Jan 21, 2003 this sequence version replaced gi:27808693.
Location/Qualifiers
GTGACAGCACCTTCAGCTTCAAATATATCATTTAGAGAGATTAAAAAATGGTTCTGCTAA
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/gene="Zarl"
/note="oocyte-specific"
/codon_start=1
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Wu,X. and Matzuk,M.M.
Direct Submission
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Baylor Plaza, Houston, TX 77030, USA
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 5, clone RP24-506B15
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LMAAEYVDSHQRAQLMALLSRWGPRSVSSBDAAVQVNBPRBASVQCSLGRRTLQPAGC
SASPDRASGSTREPERPRAARKAVPQPPRSEEGGVVQAAQQAGWBQQPPPBRNSVAAMQSEB
GSEBPCPAAEWAQDPGDSDAPRDQASPQSTEQDKERLRFQFLEQKYGYYHCKDCKKRW
ESAYWWCVQTSKVYPKQFCRVCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
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                                               'protein_id="AAO24708.1"
'db_xref="GI:27808694"
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                                Submitted (08-AUG-2004) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Ull 4, 2004 this sequence version replaced gi:46240945. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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g of 1689 bp in length
t unknown length
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g of 4441 bp in length
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of 8750 bp in length
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18 14434: contig of 2037 bp in length
15 144534: gap of unknown length
5 144954: contig of 420 bp in length.
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of 3204 bp in length
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/clone="RP24-506B15"
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Sciurognathi; Muridae; Murinae; Mus
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Submitted (27-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                        ACCGGGCCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
                                                                                                                                                                                                                                                                                                        CAGCCACCAGGGGACAGGTCATGGCCCTGCTGTCGCGGGATGGGTCCCCGGTCAG
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                                                                                                                       TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGGCCAGGGGCTGCCG
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                                                                                                                                                                           ACCCGCGCCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
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Mammalla; Eutheria; Rodentia;
1 (bases 1 to 200535)
Van Hellmond, Z.
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Aller, B. Linton, L., Bastaen, V., Boguslavkiy, L., Boukhgalter, B. Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Chang, J., Chack, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardhan, S., Gorde, S., Goyette, M., Gardan, L., Garand-Plerre, N., Gandos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Langos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Landors, T., Landers, T., Lebloczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marthews, C., McCarthy, M., McWan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McWan, P., Major, J., Marquis, N., Matthews, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogov, P., Roman, J., Robetti, M., Spencer, B., Stange-Thomann, N., Stolmbback, R., Santos, R., Schauer, S., Schupback, R., Tavers, M., Travers, M., Tander, R., Wwan, D., Ye, W.J., Young, G. Suhnisas, O., Subnek, L., Zimmer, A. and Zody, M.
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he 5 clone RP24-228B12 map 5, *** SEQUENCING
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 193274)
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CTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGC
                                                                                    GCAGACACCCAAGGAGGAGGAGGAGCCCGGGCATCCTCGGGGAACCCGGAACCGGAAGCC
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house moüse)
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Mus musculus chromosome 5, clone RP24-228B12
Unpublished
2 (bases 1 to 193274)
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Direct Submission
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                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ame. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with colly a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMEL; Sw., SWISSPROT; Tr:, TREMBL; Wp., WORWEP; Information on the WORWEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-384C22 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong.

VECTOR: PBACa2:

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = as compressions and repeats; all regions were covered by the rase one plasmid subclone or more than one MJ3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a NAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

Location/Qualifiers
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On Nov 28, 2002 this sequence version replaced gi:22204349.
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                                                                                  Center: Wellcome Trust Sanger Institute
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                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Birren, 320 Charles Street, Cambridge, MA U2141, USA

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Streen, 320 Charles Street, Cambridge, MA U2141, USA

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

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Vo, A., Wilson, B., Wuk, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,

Direct Sumission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Max 24, 2004 this sequence version replaced gi:44886211.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence as soon as it is available and the accession number will be preserved.

* 13442 23441 bp in length

* 23442 23541: gap of unknown length

* 31362 31461: gap of unknown length

* 40410 40509: gap of unknown length

* 40410 40509: gap of unknown length

* 83304 83303: contig of $2526 bp in length

* 190030 109129: contig of $55282 bp in length
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Center: Whitehead Institute/MIT Center for Genome Research
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unknown length
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164511: gap of unknown leng
193274: contig of 28763 bp
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                                                                REFERENCE
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map="5"

ORIGIN

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Rattus norvegicus clone CH230-159N5, WORKING DRAFT SEQUENCE.
AC126519
AC126519.3 GI:25138273
AC126519.3 GI:25138277
HTG, HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                             126719 FCCTTATCCGCAGGCCACCAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG
                                                                                                                                                                                                                                                                                                                126899 CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACT
                                                                                                                                         63 TCCTTATCCGCAGGCCACCAAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG
                                                                                                                                                                                                            123 ACCCGCGCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
                                                                                                                                                                                                                                                                               CAGCCACCAGCGGGCACAGCTCATGGCCCTGTCGCGGATGGGTCCCCGGTCAG
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                                                                      3 GGCGGCCGAGGCGCGCGGCACGCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA
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                                       Gaps
Length 193274;
                                      18;
                                    Indele
                                      22;
   DB 2;
Score 689.8; DB 2;
Pred. No. 5.9e-133;
0; Mismatches 22;
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   54.0%;
95.0%;
                  Best Local Similarity 95.0 Matches 761; Conservative
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KEYWORDS
SOURCE
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MATTONS ALTHOUSE 1. CANAGE WILLOW. M. ADMINION. S. Addame. C., Alder. J., Althor. C., Allen. H., Algarcooks, A., Main. A., Anguinon. D., Anguinol. W. Althor. C., Allen. H., Algarcooks, S., Main. A., Anguinol. D., Anguinol. W. Anguinol. W. Bard. B. Band. M. Sand. B. Band. B
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* NOTE: Estimated insert size may differ from sequence length

* NoTE: Estimated insert size may differ from sequence length

* NoTE: This is a 'working draft' sequence. It currently

* consists of I contigg. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

I 235390 contig of 235390 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                     Conter clone name: CH230-159N5
Center clone name: CH230-159N5
Assembly program: Phrap; version 0.990329
Consensus quality: 218035 bases at least Q40
Consensus quality: 218057 bases at least Q30
Consensus quality: 219408 bases at least Q20
Estimated insert size: 221324; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 TCCTTATCCGC---AGGCCACCACAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGGGGGGGAGGGGGGAGGCGCATGTTCCCGGGGAGCACGTTCCACCCTGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 628; DB 2; Length 235390;
Pred. No. 4.18-120;
0; Mismatches 90; Indels 6;
                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .235390
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .228048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end sequence:BH321015"
232121. .235390
/note="wgs_end_extension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_end_extension
clone_end:T7"
complement(4755..38027)
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end_sequence:BH321013"
complement(227221, .228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CH230-159N5"
                                                                                                                                                                                                                           Center project name: GZCZ
                                                                                                  Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.1%;
Matches 708; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
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Direct Submission
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                         27049 CGCCCTGTACTCGCCCGTGACCTTCGGTGGCCTCTCCTCCTCGTGGAGGTTGCGGGGA 26990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26989 CAGGCAGACGCCCACGAAGGGAGAGGGAGACCGGCACCCACGGGGACCCCGGGAACCCCGA 26930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26812 GGCGGCGATGCAGTCTGAGCCCCGGGAGTGAGGAGCCACCTCCTGCTGTTGGAGGATGGCTCA 26753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26929 GCCGGGAGAGGTGGCAGTGATGAAAGCAGTCCCCCAGCCGCAGAGCGAGGAGGGCGACGT 26870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26869 CCAGGCTGAAGGGCAGGATG---GGCAGGAGCAGCCACCGGGGAGGACCGGACAGTGT 26813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC125993 237695 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-74L11, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629
                                                                                                                                                                                                                     300 ACTCGGGCGCCGCACGCTGCAGCCTGCAGGTGCCGAGCCCAGCCCCGACGCCCGGATCGGG 359
                                                                                                                                                                                                                                                                                                                                              360 TTCCTGTCAACCCCGTGGCCACGCCGCGCGCGGGAGATCCCCGCGATCCTGGCAGACCGT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 AGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGCAGACACCCACGAAGGGAGAGAGGCCCGGCATCCTCGGGGACCCGGGAACCGGA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGCCGATGCAGTCTGAGCCTGGGAGCGAGGCCATGTCCTGCCGCAGAGATGGCTCA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 GGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 GCCGAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAAGGGGGGGATGT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 TCAGGCTGCAGGCCAGGCCGGGTGGGAGCAGCCACCACCACCGGAGGACCGGAACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC125993.3 GI:30522839
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26692 CAAGGAGCCCTGCGTTTCCAGGT 26669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             780 CAAGGAGCGCCTGCGTTTCCAGTT 803
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AC125993/c
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KEYWORDS
SOURCE
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, J., Jackson, J., Jackson, J., Jackson, R., Jacob, L., Jiang, H., Levan, J., Lewis, L., Liu, Y., Johnson, R., Johnson, R., Jolivet, A., Karpathy, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, J., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R., Ju, X., Ma, J., Liu, Y., Loulseged, H., Lozado, R., Ju, X., Ma, J., Liu, Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, R., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Morgan, M., Morris, K., Mortin, K., Martin, R., Martin, S., Morgan, M., Morris, K., Mortin, K., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, S., Munchas, J., Parks, K., Parsarley, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Reigh, R., Reilly, B., Reilly, M., Rachlin, E., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Saredy, R., Rose, R., Ruiz, S. J., Shetty, J., Shvartsbeyn, A., Saredy, R., Strong, R., Sutton, A., Sorelle, R., Sorelle, R., Sutton, A., Sorelle, R., Wallam, G., Wallam, G., Wallam, B., Walliams, G., Walleren, B., Walliams, G., Waller, R., Walliams, G., Walleren, B., Waller, R., Walliams, G., Waller, R., Walliams, G., Waller, R., Walliams, G., Wallers, R., Walle, S., Yen, J., Yoon, U., Yu, Weish, R., Shate, S., Sander, S., Shon, H., Walliams, G., Wallers, R., Walle, R., Walliams, G., Wallers, R., Walle, D., Waller, R., Walle, S., Yen, J., Yoon, U., Yu, Weish, R., Walle, D., Waller, R., Walle, M., Walle, R., Walle, R., Shate, M., Shate, S., Sander, S., Sa
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On May 10, 2003 this sequence version replaced gi:23056451.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Direct Submission
Submitted (O2-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 23765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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------ Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 229641 bases at least Q40
Consensus quality: 231444 bases at least Q30
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Center code: BCM
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Center project name: GGIZ
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See al to 262139)

Muzny, D. Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alebrooke, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Bryant, N., Blabry, C., Burch, P., Burrell, K., Carleron, E.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, T., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chen, R., Chen, R., Chen, M., Davis, C., Cookrell, R., Cock. C., Cookrell, R., Cock. Durd, M., Durbin, R., Duval, B., Eaves, V., Daylan, Robert, P., Dugan-Rocha, S., Dunn, A., Durbin, R., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Carrer, T., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Carner, T., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Garrer, T., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gabrejon, R., Haaland, W., Hanilton, K., Harlak, P., Haaland, W., Hanilton, K., Hernandez, J., Harlak, P., Haaland, W., Hanilton, R., Hernandez, J., Hanlak, R., Hanlak, S., Hulyk, S
                                                                                                                                                                                                                                                                                                                                                                                                                        gaicecarigacrigericecretagacegacerececaragacacraagas 122237
                                                                                                                                                                                                                  AC127083 262139 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-69F8, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                               720 GGACCCCCGGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGA
                           600 TCAGGCTGCAGGCCGGGCTGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGT
                                                                                                                                                                                                                                                                                    GGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGGCCATGTCCTGCCGCAGAGATGGCTCA
CAGGCAGACACCCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCCGGGAACCGGA
                                                                                           540 GCCGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGT
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AC127083.3 GI:24635317
HTG; HTGS_PHASEL; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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KEYWORDS
SOURCE
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                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ONDE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
       Consensus quality: 212679 bases at least Q20
Estimated insert size: 242796; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Pred. No. 4.1e-120;
0; Mismatches 90; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. 237695
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-74111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end sequence: BH339391"
complement (234275. .235086)
/note="clone_boundary
clone_end: Spē
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/note="wgs end_extension
clone_end:T7"
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/note="clone_boundary
clone_end:T7
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end_sequence:BH339393"
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Matches 708; Conservative 0
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236614 GGACCCCAGTGACGTGCCTCTAGAGACCGGGCCTCCCCACAGAGCACTGAGCACGGGA 236555
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Best Local Similarity 88.1
Matches 708; Conservative
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260400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 6, 2002 this sequence version replaced gi:23269432.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold'). Mithin each contig-scaffold') by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
             Reilly, B. Reilly, M. Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbern, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, Taylor, T., Thomas, N., Thomas, S., Tingey, A., Treios, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wallson, R., Waren, R., Wei, K., While, F., Willson, R., Waczen, R., Wei, X., Wholey, K., Wilght, D., Wright, D., Wright, R., Wul, Yakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Swith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-JUD-2002) Human Genome Sequencing Center, Department
Submitted (13-JUD-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 262139)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Phrap, version 0.990329
Consensus quality: 200303 bases at least Q40
Consensus quality: 206134 bases at least Q30
Consensus quality: 205370 bases at least Q20
Stimated insert size: 207464; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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4662: gap of unknown length
259056: contig of 254394 bp in length
259156: gap of unknown length
260299: contig of 1143 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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COMMENT

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0300 260399; gap of unknown length
0400 262139; contig of 1740 bp in length.
Location/Qualifiers
1. .262139
/organism="Rattus norvegicus"
/mol type="genomic DNA"
/db xref="taxon.10116"
/clone="CH230-69F8"
36039. .38559
/note="wgs contig"
108494. .109772
/note="wgs contig"
172942. .174088
/note="wgs contig"
202428. .204028
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N. Submitted (13-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 AC108848 220894 bp DNA linear HTG 13-MAR-2004 Mus musculus chromosome 5 clone RP23-300K5 map 5, WORKING DRAFT SEQUENCE, 40 unordered pieces.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 220894)
Birran, Bairran, B. Birran, B. Birran, B. Mus musculus chromosome 5, clone RP23-300K5
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                                                                                                                                                                                                      AC108848
AC108848.3 GI:45430126
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                     236554 CAAGGAGGCCTGCGTTTCCAGGT 236531
780 CAAGGAGCGCCTGCGTTTCCAGTT 803
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AC108848/c
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KEYWORDS
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COMMENT

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                                                              Center: Whitehead Institute/ MIT Center for Genome Residente: Whitehead Institute/ MIT Center for Genome Residente: Whitehead Institute/ MIT Center for Genome Residente: Code: WIBR
Web Site: http://www-seq.wi.mit.edu
Web Site: http://www-seq.wi.mit.edu
Center: Sequence submissions@genome.wi.mit.edu
Center project Information
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Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 200302 bases at least Q30
Consensus quality: 200318 bases at least Q20
Insert size: 203348; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
                Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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27699 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG 27640
                                                                                                                                                                                                                                                                                                                                                                            27164 ACCCGGGAACCGCAGCCGAGAGAGGGGGCGTGAGGAAAGCGGTCCCCCAGCCGCAAGC 27105
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 1275)
Wu, X., Viveiros, M.M., Eppig, J.J., Bai, Y., Fitzpatrick, S.L. and Matzuk, M.M.
Zygote arrest 1 (Zarl) is a novel maternal-effect gene critical for the occyte-to-embryo transition
Nat. Genet. 33 (2), 187-191 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY191416 12-MAR-2003
Homo sapiens zygote arrest 1 (ZAR1) mRNA, complete cds.
                                                                                   27639 ACCGGGCCCCCCCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
                                                                                                                                               CAGCCACCAGCGGGCACAGCTCATGGCCCTGTCGCGGATGGGTCCCCGGTCAG
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Clone="RP23-300K5"
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/mol type="genomic DNA"
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Kits, such as nucleic acid arrays, comprising a majority of 
humanexons or transcripts, for detecting expression and other uses
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Homo.
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18.7%; Score 239.2; DB 6
21 Similarity 86.2%; Pred. No. 2.9e-39;
276; Conservative 0; Mismatches 43
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PE Corporation (NY) (HS)
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    .366
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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RCLEABASPCSABASLSPPGDEVLDGYVPPACPPCSYRYPYPAATKGKGAAGGSWQQRG
RGCLPASSPCSABASLSPPGDEVLDGYVPPACPDSYQRERLMALLAQVGPGLGPPARRAG
SCCDVAVQVSPRIDAAVQCSLGRRTLQRRARDPESPAGPGAEGTTGGGSFSQQPSRRGL
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RLQGPEEGEVWTKKAPRRPQSDDGBAAQAAVRASWEQPADGPELPPREAQEGBAAPRS
ALSPSPQQPPSARARDGGDBRAAVARGEPSPRSPELGKERLRPQFLEQKYGYYHCKD
CNIRWESAYWCVQGTNKYYFKQFCRTCQKGYNPYRVEDITCQSCKQTRCSCPVKLRH
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Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
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/protein id="AAR37039.1"
/brotein id="AAR37039.1"
/db.xref="gygote arrest"
/db.xref="gygote"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY283177 963 bp mRNA linear VRT 21-AUG-2003 Takifugu rubripes zygote arrest 1 (Zarl) mRNA, complete cds. AY283177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Terraodontidae; Takifugu.

[ (bases 1 to 963)
Wu.X., Wang, P., Brown, C.A., Zilinski, C.A. and Matzuk, M.M.
Zygote arrest 1 (zarn) is an evolutionarily conserved gene expressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                                                                                                                                                                                                              832
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USA
                                                            654 GAGAGCGCCTACGTGTGTGTGCAGAAAACCAATAAGGTG-TACTTCAAGCAGTTCTG
                                                                                                                                                               976 TANANGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCCA
                                                                                                                                                                                                                                                                                                                             1036 TCGGCAAGACTTGTCTGGGAGATGCAAGACACCCTGTGCTGCGACAGCACCTTCAG
                                                                                                                                CCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTTG
                                                                                                                                                                                                                                                                                   773 CAAGCAGACGAGATGCGCGTGTCCTGTCAAACTGCGTCACGTTGACCCCCAAGAGGCCCCA
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Pred. No. 4.8e-30;
0; Mismatches 82;
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/organism="Takifugu rubripes"
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Submitted (24-APR-2003) Pathology,
Baylor Plaza, Houston, TX 77030, U.
Location/Qualifiers
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/note="maternal factor"
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/db_xref="taxon:31033"
1. .963
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75.4%;
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Wu,X. and Matzuk,M.M.
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20 (Bases 1 to 1052)
Wu,X. and Matzuk,M.M.
Direct Submission
Submitted (24-APR-2003) Pathology, Baylor College of Medicine, One
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(basea 1 to 1052)

Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M. Expecsed in Vertebrate ovaries

Expressed in Vertebrate ovaries

Biol. Reprod. 69 (3), 861-867 (2003)
ACCGTCAAGATTTGTGCGGTAGATGCAAAGGCAAACGCCTGTCCTGTGACACTTTTCA
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                                                                            GCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTT
                                                                                                                                                                             GTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAAACGCCCCC
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Xenopus laevis zygote arrest 1 (Zarl) mRNA, complete cds.
AY283176
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Xenopus laevis
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/protein_id="AAP37038.1"
/db_xref="G1:30908935"
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Location/Qualifiers
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/note="maternal factor"
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/db_xref="taxon:8355"
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Matches 254;
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PUBMED
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AUTHORS
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JOURNAL
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AY283176
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                                                                                                                                          GCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTG
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/product=12xgote arrest 1"
/product=12xgote arrest 1"
/protecin id="App31040.1"
/bc xref="G1:30908939"
/fb xref="G1:30908939"
/fb xref="G1:30908939"
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Submitted (24.APR-2003) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Location/Qualiflers
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Gypriniformes; Cyprinidae; Danio.

I (basea L to 1084)

Wu, X., Wang, P., Brown, C.A., Zilinski, C.A. and Matzuk, M.M.
Zygote arrest 1 (zarl) is an evolutionarily conserved gene axpressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
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Danio rerio zygote arrest 1 (zar1) mRNA, complete cds.
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SOUTHERNIES	ΙD	AAD00294	ADJ63191	ABZ24589	ADJ63164	ADJ63200	ADJ63208	ABZ24590	ADJ63203	ADJ63174	ABZ24591	ADJ63175	ADJ63201	ADJ63193	ADJ63211	ADJ63194	ADJ63198	ADJ63196	ABZ24592	ADJ63204	ADJ63176	ADJ63209
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de	Query Match	99.1	97.5	96.6	96.6	75.3	62.6	62.6	62.6	62.6	59.0	59.0	49.2	27.6	21.4	16.1	15.3	15.2	10.5	10.5	10.5	7.7
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ALIGNMENTS

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AAD00294 standard; cDNA; 1276

RESULT 1

Oocyte-specific; ovary; O1-180; mouse; gynaecological; treatment; screen; cell proliferative disorder; cell degenerative disorder; contraceptive; modulator; signalling pathway; human infertility; cancer; ovulation; ss. The present sequence is the cDNA encoding the mouse oocyte-specific protein 01-180, expressed in the oocytes of primary (one-layer) preantral O1-180, O1-184 and O1-236 polypeptides and nucleic acids encoding them, useful for evaluating potential contraceptives to block ovulation in a reversible manner. "Mouse oocyte-specific protein, 01-180" Mouse oocyte-specific 01-180 cDNA clone. Location/Qualifiers 28. .1113 (BAYU) BAYLOR COLLEGE MEDICINE. Claim 2; Fig 1; 54pp; English. 98US-0106020P. 99WO-US025209 /*tag= a /product= ' 05-SEP-2000 (first entry) WPI; 2000-350684/30. P-PSDB; AAY70948. Matzuk MM, Wang P; WO200024755-A1. 28-OCT-1999; 28-OCT-1998; 04-MAY-2000 AAD00294; Mus sp. Key

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17-DEC-2002; 2002US-0434165P.
13-JAN-2003; 2003US-0439781P.
23-JAN-2003; 2003US-0442164P.
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follicles through ovulation. It provides in vitro and in vivo reagents for studying ovarian development and function. This sequence has ynaecological and contraceptive activity. Agents which modulate 01-180, 01-184 and 01-236 may be used to treat cell proliferative or degenerative disorders, associated with abnormal expression of these ovary specific sequence can be used as reagents to evaluate potential contraceptives, to block ovulation in a reversible manner. It is also used to screen for genetic mutations in signalling pathways, that are associated with some forms of human infertility or gynaecological
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/product= "Murine O1-180"
/transl_except= (pos:182. .184,aa:Ser)
/transl_except= (pos:1004. .1007,aa:Phe)
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                                                            specific (also known as zygote arrest 1 - Zarl) proteins and nucleoplasmin (Npm2) proteins. The DNA and protein sequences of the invention are useful for inhibiting or enhancing early embryogenesis by disturbing the maternal genome. The DNA and protein sequences are also useful for screening mutations in components of those signalling pathways that are associated with some forms of human infertility or gynaecological cancers. The present DNA sequence encodes a Zarl protein.
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                                       the amino acid and coding sequences
                                                                                                                                                                                                                                                Sequence 1260 BP; 261 A; 390 C; 395 G; 214 T; 0 U; 0 Other;
SEQ ID NO 28; 219pp; English
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Matches 1257; Conservative
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17-SEP-2002; 2002US-0411262P.
17-BC-2002; 2002US-0434165P.
13-JAN-2003; 2003US-0439781P.
23-JAN-2003; 2003US-0442164P.
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The present sequence is that of murine ovary-specific O1-180 cDNA obtained from a mouse ovary cDNA library. O1-180 clones were initially identified in a subtractive hybridisation screen using ovaries from GdE9 thockout and wild-type mice. The O1-180 gane (see ABZ24590) on chromosome is also provided. Loss of O1-180 casults in female infertility and subfertility. The invention provides ovary-specific and oocyte-specific murine and human O1-180, O1-184 and O1-236 polymoleotides and control of colypeptides. These genes and their protein products appear to relate to various cell proliferative or degenerative disorders, especially those involving ovarian tumours, such as germ line tumours and granulosa cell cumours, or infertility, such as premature ovarian failure. The invention provides a method for detection of a cell proliferative or degenerative contents, or infertility, such as premature ovarian failure. The invention provides a method for detection of a cell proliferative or degenerative coll-184 or O1-236. It also provides a method for treating such disorders of o1-184 or O1-236, and a method of screening for compounds that content which suppresses or enhances the respective activities of interact and/or modulate the expression or activity of the ovary-specific genes. These compounds are possible contraceptive or fertility enhancing agents. The modulator is preferably a polypeptide, small molecule or
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Best Local Similarity 99.3%;
Matches 1250; Conservative
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CTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCC
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2002US-0411262P.
2002US-0434165P.
2003US-0439781P.
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                                 New isolated ovary-specific genes e.g. 01-180, 01-184 or 01-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by 01-180, 01-184 or 01-236 proteins.
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Matches 1250; Conservative
2003-865579/80
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13-JAN-2003; 2003US-0439781P.
23-JAN-2003; 2003US-0442164P.
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in inhibiting or enhancing early embryogenesis or treating cell
proliferative or degenerative disorders which are mediated by 01-180,
184 or 01-236 proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 962.2; DB 10; Length
Pred. No. 1.1e-218;
0; Mismatches 143; Indels
                                                                                                         Claim 1; SEQ ID NO 37; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.3%;
Best Local Similarity 87.7%;
Matches 1110; Conservative
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therapy; chromosome 5; gene; ds.
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                                                                                                        specific (also known as zygote arrest 1 - Zarl) proteins and mucleoplasmin (Npm2) proteins. The DNA and protein sequences of the invention are useful for inhibiting or enhancing early embryogenesis by disturbing the maternal genome. The DNA and protein sequences are also useful for screening mutations in components of those signalling pathways gynaccological cancers. The present DNA sequence represents exon 1 from a Zarl gene.
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New isolated ovary-specific genes e.g. Ol-180, Ol-184 or Ol-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by Ol-180, Ol 184 or Ol-236 proteins.
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                                                                                                                                                                                                                          Sequence 814 BP; 135 A; 285 C; 290 G; 104 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Score 799.4; DB 10; Length
Pred. No. 5e-180;
0; Mismatches 1; Indels
                                                                      Disclosure; Fig 19; 219pp; English.
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Best Local Similarity 99.9%;
Matches 800; Conservative
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subtractive hybridisation screening using ovaries from Gdf9 knockout mice and wild-type mice. Ol-180 cDMA (see AB224589) was then used to isolate the Ol-180 gene from a genomic library generated from mouse 1298vy strain. Loss of Ol-180 results in female infertility and subfertility.

The invention provides ovary-specific and occyte-specific murine and muran and ol-180, Ol-184 and Ol-218 polymucleotides and polypeptides. These genes and their protein products appear to relate to various cell genes and their protein products appear to relate to various cell proliferative or degenerative disorders, especially those involving ovarian tumours, such as germ line tumours and granulosa cell tumours, or infertility, such as germ line tumours and granulosa cell tumours, or infertility, such as premature ovarian failure. The invention provides a cheovary, which is associated with the expression of Ol-180, or Ol-236. It also provides a method for treating such disorders by using an agent which suppresses or enhances the respective activities of Ol-180, or Iss or Ol-236, and a method of screening for compounds that interact and/or modulate the expression or activity of the ovary-specific genes. These compounds are possible contraceptive or fertility enhancing agents. 3232 3172 2572 2632 2692 2752 2812 2872 2932 2992 3052 GAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCAAGCGAGGAGGGCGATGTTCA 3112 ö 482 542 602 662 GGCGATGCAGTCTGAGGCTGGGAGCGAGGGCCATGTCCTGCCGCAGAGATGGCTCAGGA 722 122 242 302 362 422 ACCCGCCCCCCCCTCCTTCCTCCCGGCTACAGACAGCTCATGGCCGCGGGAGTACGTCGA 182 62 CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCCGCGACGCCTCGGTGCACGTGCACGTTCACT CIGICAACCCCGIGGCCACGCCGGCGCCGGGAATCCCCGCGAICCIGGCAGACCGIAGC CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG 2933 CCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCCTCGAGGGTTGCGGAAGGAG GCAGACACCCACGAAGGGAAGAGGGAAGCCCGGCATCCTCGGGGAACCCGGGAACCGGAAGCC GCAGACACCCACGAGGAGAGAGAGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCC GGCTGCAGGGCAGGCCGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGC GGCTGCAGGCCAGGCCGGGAGCAGCAGCCACCACGGAGGACCGGAACAGTGTGGC CGGGCGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTC GAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCA CTGTCAACCCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGC 2513 esceseceaesceceaeacecaccarerreceseceaecacerrecaccerecere TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG 2573 TCCTTATCCGCAGGCCACCAAAGCCGGGATGGCTGGAGGTTCGGAGCCAGGGGTGCCG ACCGGGCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGGGGTACGTCGA CAGCCGTGACGCTGCGGGTGAACCCGCGCGCGACGCCTCGGTGCTGTTCACT 3 GGCGGGCGAGGCGCACGCACCCATGTTCCCGGCGAGCACGTTCCACCCTGCCCGCAA Gaps ö Sequence 6873 BP; 1716 A; 1624 C; 1697 G; 1836 T; 0 U; 0 Other; 62.6%; Score 799.4; DB 8; Length 6873; 99.9%; Pred. No. 1e-179; ive 0; Mismatches 1; Indels 0; 800; Conservative polynucleotide sequence Query Match Best Local Similarity 123 2633 2693 2753 2813 2873 2993 543 3053 603 3113 63 183 243 303 363 423 483 663 Best Local 쉽 ò à g 엄 8 엄 ò 셤 à g ò g ò g à 유 8 셤 d ò ò

The invention comprises the amino acid and coding sequences of ovaryspecific (also known as zygote arrest 1 - Zarl) proteins and nucleoplasmin (Npm2) proteins. The DNA and protein sequences of the invention are useful for inhibiting or enhancing early embryogenesis by disturbing the maternal genome. The DNA and protein sequences are also useful for screening mutations in components of those signalling pathways that are associated with some forms of human infertility or gynaecological cancers. The present nucleic acid represents a Zarl DNA 63 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCCAGGGGCTGCCG 122 3233 CCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGAACAA 3292 CCCCGGTGATTCGGATGCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAA 782 New isolated ovary-specific genes e.g. Ol-180, Ol-184 or Ol-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by Ol-180, Ol-184 or Ol-236 proteins. Gaps . ovary-specific protein; zygote arrest 1; Zar1; nucleoplasmin; Npm2; embryogenesis; mutation screening; infertility; gynaecological cancer; ds; mouse; murine. 3 GGCGGGCGAGCGCGCACCCATGTTCCCGGCGAGCACGTCCACCCCTGCCCGCA Score 799.4; DB 10; Length 6873; Pred. No. 1e-179; 0; Mismatches 1; Indels 0; Sequence 6873 BP; 1714 A; 1624 C; 1698 G; 1837 T; 0 U; 0 Other; DNA sequence #3. 0; Mismatches Claim 1; SEQ ID NO 40; 219pp; English. GGAGCGCCTGCGTTTCCAGGT 3313 Υ; Bai BP. (BAYU) BAYLOR COLLEGE MEDICINE. (AMHP) WYETH. GGAGCGCCTGCGTTTCCAGTT ; 2002WO-US013245. ; 2002US-0411262P. ; 2002US-0434165P. 17-SEP-2002; 2002US-0411262P. 17-DEC-2002; 2002US-0434165P. 13-JAN-2003; 2003US-0439791P. 23-JAN-2003; 2003US-0442164P. Query Match 62.6%; Best Local Similarity 99.9%; Matches 800; Conservative ADJ63203 standard; DNA; 6873 Mouse zygote arrest 1 (Zarl) 23-APR-2003; 2003WO-US012720 × 06-MAY-2004 (first entry) Wu Wang P, WPI; 2003-865579/80. WO2003091400-A2. 26-APR-2002; Mus musculus 06-NOV-2003 Matzuk MM, 2515 ADJ63203; seguence 723 783 RESULT 8 ADJ63203 g ò g 셤 ò

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The invention comprises the amino acid and coding sequences of ovary-specific (also known as zygote arrest 1 - Zarl) proteins and nucleoplasmin (Npm2) proteins. The DNA and protein sequences of the invention are useful for inhibiting or enhancing early embryogenesis by disturbing the maternal genome. The DNA and protein sequences are also useful for screening mutations in components of those signalling pathways that are associated with some forms of human infertility or gynaecological cancers. The present nucleic acid represents a Zarl DNA

New isolated ovary-specific genes e.g. Ol-180, Ol-184 or Ol-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by Ol-180, Ol-184 or Ol-236 proteins.

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Wang

Matzuk MM,

WPI; 2003-865579/80

(BAYU) BAYLOR COLLEGE MEDICINE (AMHP) WYETH.

26-APR-2002; 2002WO-US013245. 17-EEP-2002; 2002US-0411262P. 17-DEC-2002; 2002US-0434165P. 13-JAN-2003; 2003US-0492164P.

Claim 1; SEQ ID NO 11; 219pp; English

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Mouse zygote arrest 1 (Zarl) DNA sequence #1

(first entry)

06-MAY-2004

ADJ63174

23-APR-2003; 2003WO-US012720.

WO2003091400-A2

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06-NOV-2003

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ADJ63174 Standard; DNA; 6873

ADJ63174

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2513 GGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAGCACGTTCCACCCTGCCCGCA

3 GGGGGGGGGGGGGGGGGACGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA

Query Match 62.6%; Score 799.4; DB 10; Length 6873; Best Local Similarity 99.9%; Pred. No. 1e-179; Matches 800; Conservative 0; Mismatches 1; Indels 0;

Sequence 6873 BP; 1716 A; 1624 C; 1697 G; 1836 T;

sequence

2573 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTTGAAGGTTCGGAGCCAGGGCTGCCG

TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG

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The present sequence is that of a pseudogene isolated during the cloning of novel murine ovary-specific gene O1-180 (see AB224590). The major difference between the O1-180 gene and pseudogene is a 13-nucleotide gap in exon 1 of the pseudogene. Which is expected to cause a frameshift and carly termination in exon 2 of the pseudogene. The sequences of exon 2 are identical in the O1-180 gene and pseudogene. The sequences of exon 2 are identical in the O1-180 gene and pseudogene, and there are single by cutations in exons 3 and 4. The invention provides ovary-specific and cocyte-specific murine and human O1-180, O1-184 and O1-236 polynucleotides and polypeptides. These genes and their protein products opynucleotides and polypeptides. These genes and their protein products especially those involving ovarian tumours, such as germ line tumours and farmulas cell tumours, or infertility, such as premature ovarian callure. Diagnostic and therapeutic methods using the genes, polypeptides and modulator compounds are provided. Modulators also have contraceptive or fertility enhancing activities
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Pred. No. 5.9e-169;
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17-DEC-2002; 2002US-0434165P.
13-JAN-2003; 2003US-0439781P.
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17-SEP-2002; 2002US-0411262P.
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13-JAN-2003; 2003US-0439781P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated ovary-specific genes e.g. 01-180, 01-184 or 01-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by 01-180, 01-184 or 01-236 proteins.
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Pred. No. 1.4e-73;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; zygote arrest 1; Zarl; nucleoplasmin; Npm2; mutation screening; infertility; gynaecological cancer;
<u>AAAGTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAAC</u>
                                                                                                                                                                          GCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCA
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; 2002US-0411262P.
; 2002US-0434165P.
; 2003US-0439781P.
; 2003US-0442164P.
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Best Local Similarity 95.3
Matches 282; Conservative
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Sequence 1052 BP; 298 A; 228 C; 299 G; 227 T; 0 U; 0 Other;

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1085 AGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGG 1144
                                                                                                                                          1145 GCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCTTCCCAAATTCTT 1204
                                            1025 AAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGAC 1084
TGTCAAAGTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCT 1024
                                                                                                       70 AAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAATGCTTGTCCTGCGAC 129
                                                                                                                                                                190 GCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCCCTTTCCCATTTCCAAATTCTT 249
                     69
                                                                                                                                                                                         CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 1260
                                                                                                                                                                                                                                                                                                                                                                     ovary-specific protein; zygote arrest 1; Zar1; nucleoplasmin; Npm2; embryogenesis; mutation screening; infertility; gynaecological cancer;
             10 TTTCAGAGTTGTAAAAGAACTAGAGTGTGCCTGCCCAGTCAGACTTCGCCACGTGGACCCT
                                                                                                                                                                                                       250 CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 305
                                                                                                                                                                                                                                                                                                                                                Frog zygote arrest 1 (Zarl) protein coding sequence.
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17-SEP-2002, 2002US-0411264P.
17-DEC-2002, 2002US-0434165P.
13-JAN-2003, 2003US-0439781P.
23-JAN-2003, 2003US-0442164P.
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P-PSDB; ADJ63195.
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The invention comprises the amino acid and coding sequences of ovary-specific (also known as zygote arrest 1 - Zarl) proteins and mucleoplasmin (Npm2) proteins. The DNA and protein sequences of the invention are useful for inhibiting or enhancing early embryogenesis by disturbing the maternal genome. The DNA and protein sequences are also disturbing the material momerate of those signalling pathways that are associated with some forms of human infertility or gynaecological cancers. The present DNA sequence encodes a Zarl protein.

New isolated ovary-specific genes e.g. Ol-180, Ol-184 or Ol-236, useful in inhibiting or enhancing early embryogenesis or treating cell proliferative or degenerative disorders which are mediated by Ol-180, Ol-184 or Ol-236 proteins.

Claim 1; SEQ ID NO 31; 219pp; English.

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1036 TCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCACCTTCAG 1095
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                          62; Indels
Score 205.8; DB 1
Pred. No. 7.7e-39;
0; Mismatches 62
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Job time : 698 secs
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             Similarity
               Best Local Sim:
Matches 254;
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-076-556-179

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US-08-455-543A-8

US-08-455-543A-8

US-08-223-305G-8

US-08-233-305G-8

US-08-233-305G-8

US-08-490-386-8

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Maximum DB seq length: 200000000
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ALIGNMENTS

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GEOUT-745-206A-12
Sequence 12, Application US/07745206A
Facente 0.5, Application US/07745206A
Facente 0.5, Application US/07745206A
Facente 0.5, Application US/07745206A
Facente 0.5, Application Michael
APPLICANT: Harpold, Michael
APPLICANT: MCCLe, Ann.
APPLICANT: Heldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LeSalle
CITY: Chicago
STATE: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Ploppy disk
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FERRENCE/CATION DATA: 435
ATTORNEY/ARTIN INFORMATION:
NAME: Feder, Scott B
FERCOMMUNICATION INFORMATION:
TELEPHONE: 3132-728-742
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERIFICS:
LENGTH: 3467 Asse pairs
TYPE: NUCLEC ACID
TYPE COMPUTER: ADDRESS: UNANOWN
TOPOLOGY: ``

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SEQUENCE CHARACTERISTICS
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 663 GGCGAT 668
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 423 CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
 GCAGACCCCACGAAGGGAGAGGGGCCCGGCCATCCTCGGGGACCCGGGAACCGGAGCC
 543 GAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCA
 GGCTGCAGGGCAGGCCGGGTGGGAGCAGCCACCACCACCGGAGGACCGGAACAGTGGCC
 Gaps
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Blis, Steven
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
 ..
0
Score 54; DB 1; Length 5467;
Pred. No. 0.00039;
0; Mismatches 195; Indels
 SUFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
 E: Brown, Martin, Haller & McClain
1660 Union Street
 NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHORE: (619)238-0999
TELEPAX: (619)238-0929
TELEPAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 12:
 US 07/745,206
 Sequence 12, Application US/08311363 Patent No. 5876958
 STRET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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COMPU
 Query Match
Best Local Similarity 46.7%;
Matches 171; Conservative
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
 3160 TĠAĠĀŢ 3165
 663 GGCGAT 668
 US-08-311-363-12
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 363 CTGTCAACCCCGTGGCCACGCCGGCGCGGAGATCCCCGCGATCCTGGCAGACCGTAGC
 543 GAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCGCGAAGCGAAGGAGGGGGATGTTCA
 3040 ccecedadecedeacacededadadecedecedecededeacededecedadedeech
 GGCTGCAGGGCAGGCCGGGTGGGAGCAGCCACCGGAGGACCGGAACAGTGTGGC
 2860 ceacceaegecceaegececeaegecegecegecegecaecegececegecececegearda
 423 CCCGTTCTCGTCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
 483 GCAGACACCCACGAAGGGAAGGGGAGCCCGGCATCCTCGGGGGACCCCGGGAACCGGAGCC
 ;
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 join(144..3164, 3168..3245, 3249..3386, 3390
..3392, 3396..3488, 3495..3539, 3543..3581, 3585
..3587, 3591..3626, 3630..3689, 3693..3737, 3744
..3746, 3750..4823, 4827..4841, 4845..5006, 5010
..5096, 5100..5306, 5310..5366, 5370..5465)
 Length 5467;
 4.2%; Score 54; DB 2; Length 546
46.7%; Pred. No. 0.00039;
tive 0; Mismatches 195; Indels
 Version #1.25
 GENERAL INPORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFILINGER, F.
APPLICANT: SCHEIFILINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
 CORPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463

FILING DATE:
 US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
 STREET: 1800 Diagonal Road, St. CITY: Alexandria STATE: VA
 MOLECULE TYPE: DNA (genomic) FEATURE:
LENGTH: 5467 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
 Query Match
Best Local Similarity 46.7'
Matches 171; Conservative
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 465 GGAGGTTGCGGGAGGCAGGCAGACACCCACGAAGGGAGAGGGGGGGCCCGGCATCCTCGGG 524
 525 GACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAGCGGTCCCCCAGCCGCGAAG 584
 585 CGAGGAGGCGATGTTCAGGCTGCAGGCCGGGTGGGAGCAGCAGCACCACCACCGGA 644
 645 GGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCATGTCCTGC 704
 705 CGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCA 764
 765 AAGCACGGAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTA 824
 Gaps
 ö
 Query Match 4.2%; Score 53.2; DB 1; Length 7 Best Local Similarity 6.5%; Pred. No. 0.00072; Matches 25; Conservative 202; Mismatches 155; Indels
 GENERAL INFORMATION:
APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
TITLE OF INVENTION: THEIR USE
 30472/114 IMMU
 AFFLA......FILING DATE:
PILLING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 836-9300
TELEFAX: (703) 683-4109
 E: SPRUNG HORN KRAMER & WOODS 660 White Plains Road
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
 1028 AATICIGIGAGCGIATGGCAAA 1007
 825 CTATCACTGCAAGGACTGCAAA 846
 5-08-456-200B-11
Sequence 11, Application US/08456200B
Patent No. 6229000
 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HO
STREET: 660 White Pl
 TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZGpt-F18
 CITY: Tarrytown STATE: New York
 US-08-232-463-14
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1636 GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGTGCCGGGAGGAGCGGCCGCGGCGGCGGCAC 1695
 1753 GGCCCAGGCCCCGAGGGCGGCCGCCGCCACCACGCGCGCGCTCCCCGGAGGAGGCGGCC 1812
 1813 GAGCGGGAGCCCCGACGCCACCGCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 1872
 1696 CGCA-GCCACAGCAAGGAGGCCGCGGGGCC--CCCGGAGGCGCGGGAGCAGCGCGCGGCGGA 1752
 1873 GGCGCCAAGGGCGAGCGGNGNGCGCGGCACCGCGGCGCCCCGAGCGGGGCCCCGGGAG 1932
 1933 GCGGAGAGCGGGGAGGAGCCGGCGGCGGCACCGGGCCCGGCACAAGGCGCAGCCTGCT 1992
 490 CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGGAG
 1993 CACGAGGCTGTGGAGAAGAGACCACNGAGAAGGAGGCCACGGAGAAGGAGGCTGAGAT 2051
 370 CCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGGCGATCCTGGCAGACCGTAGCCCGGTTC
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGCCTCGGTGCAGTGTTCACTCGGGCGC
 310 CGCACGCTGCAGCCTGCAGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT
 Gaps
 3;
 Score 50.8; DB 3; Length 6232;
Pred. No. 0.0029;
0; Mismatches 215; Indels 3
 REFERENCE/DOCKET NUMBER: Bayer 8398.3-KGB TELECOMMUNICATION INFORMATION:
ZIP: 10591-5144
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: 8torage
COMPUTER: NEC POWERMATE SX/20
 APPLICATION NUMBER: US/08/456,200B FILING DATE: 31-MAY-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: BAPLICATION NUMBER: 08/094,712 FILING DATE: 19-JUL-1993 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 41 10 785
FILLING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
 APPLICATION NUMBER: 07/858,278
FILING DATE: 26-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,778
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
 REGISTRATION NUMBER: 33,141
 INFORMATION FOR SEQ ID NO: 11:
 SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
 4.0%;
 (914) 332-1700
 LENGTH: 6232 nucleotides
TYPE: Nucleotide
STRANDEDNESS: Single
 TELEFAX: (914) 332-1844
 Query Match
Best Local Similarity 48.0
Matches 201; Conservative
 COMPUTER: NEC POWERMA
OPERATING SYSTEM: DOS
 SEQUENCE CHARACTERISTICS
 TOPOLOGY: Linear
MOLECULE TYPE: CDNA
 TELEPHONE:
 US-08-456-200B-11
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 CACCEGAGGACCEGAACAGTETGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGCCAT 697
 518 CCTCGGGGACCCGGGAACCGGAGCCGAGGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGC
 179 ceccedanalceccedanacececedadacacacacacacacececececececacacas
 578 CGCGAAGCGAGGCGATGTTCAGGCTGCAGGCAGGCCGGGTGGGAGCAGCAAC
 Gaps
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Iodes, Michael J.
APPLICANT: Mendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and Norm:
 ;
0
 DB 4; Length 400;
 Score 49.6; DB 4; Length 4
Pred. No. 0.0016;
0; Mismatches 134; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998
 REGISTRATION NUMBER: 31,392
REPREMENCE/DOCKET NUMBER: 210121.417C9
TELECOMINICATION INFORMATION:
TELEPHONE: (206) 622-4900
 698 GTCCTGCCGCAGAGATGGCTCAGG 721
 359 cgccgccgacgcrgcacrcrcagg 382
 US-09-072-967-179
Sequence 179, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
 PC-DOS/MS-DOS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 Query Match 3.9%;
Best Local Similarity 49.2%;
Matches 130; Conservative
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
 TELEPHONE: (206) 622-491
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
 LENGTH: 400 base pairs
TYPE: nucleic acid
 SEQUENCE CHARACTERISTICS:
 single
 Washington
 OPERATING SYSTEM:
 linear
 ZIP: 98104-7092
 CITY: Seattle
STATE: Washingt
COUNTRY: USA
 STRANDEDNESS
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TOPOLOGY:
US-09-072-596-174
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 518 CCTCGGGGGACCCGGGAGCCGAGAGAGGTGGCCGCGGAGGAAAGCGGTCCCCCAGC 577
 179 cogcoganacogo da a conseces de contra co
 0; Gaps
 APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
 Query Match 3.9%; Score 49.6; DB 3; Length 400; Best Local Similarity 49.2%; Pred. No. 0.0016; Matches 130; Conservative 0; Mismatches 134; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/056,556 FILING DATE: 07-APR-1998
 5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
 FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
 698 GTCCTGCCGCAGAGATGGCTCAGG 721
 359 ceccecceacecrecacrercade 382
 Sequence 174, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 179, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
 (206) 622-4900
 LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 ZIP: 98104-7092
COMPUTER READABLE FORM:
 Washington
 linear
 Seattle
 RESULT 6
US-09-072-596-174
 TELEPHONE:
 US-09-056-556-179
 US-09-056-556-179
 ADDRESSEE:
 COUNTRY:
 STREET:
CITY: Se
STATE: V
 RESULT 5
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APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
UNMER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
 3.8%; Score 49; DB 1; Length 7175; 48.0%; Pred. No. 0.0091;
 Brown, Martin, Haller & McClain
 APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: BASTEM: DOS
SOFTWARE:
SOFTWARE: WS/08/455,543A
FILING DATE: MAY 31, 1995
FRIOR APPLICATION NUMBER: 08/23,305
FRIOR APPLICATION NUMBER: 08/23,305
FRIUNG DATE: April 4, 1994
FRIUNG DATE: April 10, 1992
FRIUNG DATE: April 10, 1992
FRIUNG DATE: April 10, 1992
FRIUNG DATE: April 10, 1992
FRIUNG DATE: 15-AUG-1991
FRIOR APPLICATION NUMBER: US 07/45,206
FRIUNG DATE: 30-NOV-1990
FRIUNG APPLICATION NUMBER: US 07/620,250
FRIUNG DATE: 30-NOV-1990
FRIUNG APPLICATION NUMBER: US 07/482,384
APPLICATION NUMBER: US 07/482,384
 NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMUNICATION INFORMATION:
 WOLECULE TYPE: DNA (genomic)
 1660 Union Street
 (619) 238-0999
 7175 base pairs
 TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 3'UTR
6855..7175
 TYPE: nucleic acid
STRANDEDNESS: double
 144..6857
 CITY: San Diego
STATE: California
 1..143
 Query Match
Best Local Similarity
 lineaı
 5' UTR
 USA
 ADDRESSEE:
 NAME/KEY:
 ; NAME/KEY:
; LOCATION:
US-08-455-543A-8
 LOCATION:
 NAME/KEY:
 LOCATION:
 COUNTRY:
 STREET:
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 119 crrchiccanadececicacescanacecesanicas 178
 518 CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAGCGGTCCCCCAGC 577
 578 CGCGAAGCGAGGGCGATGTTCAGGCTGCAGGCCAGGCCGGGTGGGAGCAGCAGCACCAC 637
 638 CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT 697
 0; Gaps
 APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
 Query Match 3.9%; Score 49.6; DB 4; Length 400; Best Local Similarity 49.2%; Pred. No. 0.0016; Matches 130; Conservative 0; Mismatches 134; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATYONEX/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C9
TELECOMMUNICATION:
TELECOMMUNICATION:
 6300 Columbia Center, 701 Fifth Avenue
 698 GTCCTGCCGCAGAGATGGCTCAGG 721
 359 cggcgcgacgcacrcrcagg 382
 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 8, Application US/08455543A Patent No. 5792846 GENERAL INFORMATION: APPLICANT: Harpold, Michael APPLICANT: Ellis, Steven
 SEED and BERRY LLP
 TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
 Davin C.
 LENGTH: 400 base pairs
TYPE: nucleic acid
 Washington
: USA
 linear
 Seattle
 STRANDEDNESS:
 ADDRESSEE:
STREET: 63
 US-09-072-967-179
 CITY: Sea
STATE: Wa
COUNTRY:
 US-08-455-543A-8
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us-09-830-810a-1.rni

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3048 eceleagaccededadeccecececedededeccedeccedecadaagecedadecteder 3107
 610 GGGCAGGCCGGGTGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
 2751 GAGGCCCCGGAAGGCGGAGAGCGGGAGCCCGGTGCCCGGAGGAGGAGGAGGAGGGCGCGGGCGCAAC
 2928 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC
 490 CCCACGAAGGGAAGAGGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAAGAGAG
 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGCCTCGGTGCTGCTTCACTCGGGCGC
 310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA
 370 CCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGGCATCCTGGCAGACCGTAGCCCCGTTC
 Sequence 8, Application US/08223305C
Sequence 8, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Filliams, Mark
APPLICANT: Filliams, Mark
APPLICANT: McCue, Ann
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 Length 7175;
 Score 49; DB 2; Length 717
Pred. No. 0.0091;
0; Mismatches 215; Indels
 B: Brown, Martin, Haller & McClain
1660 Union Street
 MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
 TITLE OF INVENTION: HUMAN C?
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
 3.8%;
 8:
 7175 base pairs
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 48.0
Matches 201; Conservative
 TYPE: nucleic acid
STRANDEDNESS: double
 6855..7175
 144..6857
 San Diego
California
 linear
 1..143
 92101-2926
 S'UTR
 ADDRESSEE:
 NAME/KEY:
LOCATION:
 RESULT 10
US-08-223-305C-8
 COUNTRY:
ZIP: 921
 TOPOLOGY:
 LOCATION:
 ;
LOCATION:
US-08-193-078B-8
 NAME/KEY:
 STREET:
 LENGTH:
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 490 CCCACGAAGGGAGAGGCCCGGCATCCTCGGGGACCCGGGAACCGGAGAGCGAGAGG 549
 regreegedagecracrecrecrecreargagerracgegegegecagaca 489
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC
 310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCCGACGCCCGATCGGGTTCCTGTCAA
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT
 Sequence 8, Application US/08193078B
) Patent No. 5846757
) GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Harbold, Mark
APPLICANT: Faldman, Daniel
APPLICANT: Feddman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
) NUMBER OF SEQUENCES: 29
CORRESPONDENCE 20
Mismatches 215; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
 ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
 FILING DATE: US 07/745,206
FILING DATE: 12-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
 FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/868,354
PRIUNG DATE: 10-APR-1992
PRIOR APPLICATION DATA:
 PC-DOS/MS-DOS
 0
 201; Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 USA
 ZIP: 92101
 US-08-193-078B-8
 STATE: C
 Matches
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Gaps

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 490 CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAG 549
 GTGGCCGCGAGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGGGCGATGTTCAGGCTGCA 609
 3108 CACGAGGCTGTGGAGAAGAGACCACGGAGAAGGAGCCACGGAGAAGGAGGCTGAGAT 3166
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT
 APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
CORRESPONDENCE ADDRESS:
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
 APPLICATION NUMBER: US/08/149,097D
FILING DATE: 05-NOV-1993
CLIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
PRIOR DATE: 13-JUL-1992
PRIOR APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
PRIOR APPLICATION NUMBER: US 07/968,354
 UMBER: WO PCT/US89/01408
04-APR-1989
 FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/USRG/01407
 FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
 FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
 Sequence 8, Application US/08149097D Patent No. 5874236 GENERAL INFORMATION:
 ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
CIRDDENTMARE: Patentin Pc-
 FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
 San Diego
California
 US-08-149-097D-8
 250
 STATE:
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 2868 GGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGCGCGCGCGCTCCCCGGAGGAGGCGCC 2927
 2928 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
 309
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC
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 370 CCCCGTGGCCACGCCGGCGCGGGAATCCCCGGGATCCTGGCAGACCGTAGCCCCGTTC
 3; Gaps
 Score 49; DB 2; Length 7175;
Pred. No. 0.0091;
0; Mismatches 215; Indels
 (P519739)
 OPERATING SYSTEM: DOS

CURRARE: Fast SEQ Version 1.5

CURRARE: Fast SEQ Version 1.5

CURRARD APPLICATION DATA:

APPLICATION NUMBER: US/08/23,305C

FILING DATE: April 10, 1992

APPLICATION NUMBER: US/07/45,206

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/45,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/45,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/482,384

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WS/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/03,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/03/751

FILING DATE: US/04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/176,899

FILING DATE: O4-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
 NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516
TELECOMMINICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
 MOLECULE TYPE: DNA (genomic) FEATURE:
 3.8%;
 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 7175 base pairs
 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
 Query Match 3.8
Best Local Similarity 48.0
Matches 201, Conservative
 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
 3'UTR
6855..7175
COMPUTER READABLE FORM
 144..6857
 5'UTR
1..143
 COMPUTER: IBM CO
OPERATING SYSTEM:
 NAME/KEY:
LOCATION:
 NAME/KEY:
LOCATION:
 NAME/KEY:
 ; LOCATION:
US-08-223-305C-8
 310
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Best Local Similarity 48.0
Matches 201; Conservative
 TYPE: nucleic acid
STRANDEDNESS: double
 6855..7175
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 144..6857
 San Diego
California
 1..143
 linear
 S'UTR
 CLASSIFICATION:
 FILING DATE
 LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
 92101
 TOPOLOGY:
 NAME/KEY:
 LOCATION:
 NAME/KEY:
 US-08-949-386-8
 COUNTRY:
 Query Match
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 2928 gadcogodadececacodecacedecacedecacededatecedadeaagadece 2987
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 3108 caccadedricticadadadadaccacegagaadedaccacegagaagaagadedricadar 3166
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGTCGTCGGTGCAGTGTTCACTCGGGCGC
 2811 ciccia decardada de desendos de estas de e
 370 CCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCTTC
 3; Gaps
 APPLICANT: Gillegie, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
 Length 7175;
 Score 49; DB 2; Length 717
Pred. No. 0.0091;
0; Mismatches 215; Indels
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seldman: Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-55038
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 238-099
TELEFAX: (619) 238-0662
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
 Sequence 8, Application US/08949386
Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Bilis, Steven
APPLICANT: Williams, Mark
APPLICANT: Gillespie, Alison
APPLICANT: Gillespie, Alison
 3.8%;
illarity 48.0%;
Conservative 0
 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
 3'UTR
6855..7175
 CDS
144..6857
 1..143
 Best Local Similarity
Matches 201; Conserv
 5'UTR
 FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
 ; NAME/KEY:
; LOCATION:
US-08-149-097D-8
 LOCATION:
FEATURE:
 RESULT 12
US-08-949-386-8
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 490 CCCACGAAGGGAGGGGGGGGGATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAG 549
 550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
 309
 250 GACGCTGCGGTGAACCCGCGCCGCGACGCCTCGGTGCAGTTCACTCGGGCGC
 310 cechcicacionecheconecheconecidencecidente de la contraction de
 2811 ciccia-ciccaciacicaa de a deconorio de constante de
 1928 gadcegdadececeacdeceaedecaecedecaecaedaareceaagaagaagaeceee
 2751 daddicccidaadacddadadadaddadciddaaddcaddaddaddaddaddad
 370 CCCCGTGGCCACGCCGGCGCCCGGGATCCCCGCGATCCTGGCAGACCGTAGCCCCCTTC
 Length 7175;
 0; Mismatches 215; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
 DB 3;
0.0091;
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
 Score 49;
Pred. No. (
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FILING DATE: 11-A0021994
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-A0G-1993
ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REBERENGE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 238-0999
TELEPAX: (619) 238-0929
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
 3.8%;
 MOLECULE TYPE: DNA (genomic)
 7175 base pairs
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NAME/KEY:
LOCATION:
 NAME/KEY:
LOCATION:
 ; NAME/KEY:
; LOCATION:
US-08-450-562-8
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3048 GCGGAGAGCGGGGGGGGGGGGCACCGGCCCGGCACAAGGCGCACCTGCT 3107
 3108 CACGAĞĞÇTĞTĞGAĞAAĞĞAĞACCACGGAGAAĞĞAĞĞCÇACĞGAĞAAĞAĞĞĞTĞAĞAT 3166
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
 APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Alison
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
 ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
 ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
 PCT/US92/06903
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,562
FILING DATE:
 CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/29,012
FILING DATE: 4-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/23,305
FILING DATE: 3-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 5-NOV-1993
 PAPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-UUX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
 Sequence 8, Application US/08450562
Patent No. 6096514
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 CITY: San Diego
STATE: California
 RESULT 13
US-08-450-562-8
 COUNTRY:
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2810
 2868 GGCCCAGGCCCCGAGGCGGCCGGCGCCACCACCGCGCGCGCGCTCCCCGGAGGAGGCGCC 2927
 2811 cech-eccachecanegadeccecececec--cecegadececeaecenecececece
 429
 2928 GAĞCGGĞAĞCCCCGACĞCCACCGCGCĞCĞCACCGĞĞATCCĞAĞCAAĞCAAĞGGĞTGCĞCC 2987
 2988 GGCGCCAÁGGGCGÁGCGCGCGCGCGCACCGCGGCGCCCCCGÁGCGGGGCCCCGGGÁG 3047
 3048 ecedadadecededadecedecededededecededecededadecedadecentarion
 550 GTGGCCGCGAAAAGCGGTCCCCCAGCCGCGAAGCGAAGGAGGCGATGTTCAGGCTGCA 609
 610 GGGCAGCCGGGTGGGAGCAGCACCACCACGGAGGACCGGAACAGTGTGGCGGCGAT 668
 310 CGCACGCTGCAGGGTGCCGAGCCAGGCCCCGACGCCCGATCGGGTTCCTGTCAA
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 370 CCCGTGGCCACGCCGGCGCGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCGTTC
 490 CCCACGAAGGGAAGAGGCCCGGCATCCTCGGGGACCCCGGGAACCGGAGCCGAGAGAG
 3.8%; Score 49; DB 3; Length 7175; llarity 48.0%; Pred. No. 0.0091; Conservative 0; Mismatches 215; Indels
 PFILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 02-FEB-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
PILING DATE: 04-APR-1989
PRIOR APPLICATION NUMBER: 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sciedan, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 238-0999
TELEFAX: (619) 238-0962
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
 SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 6855..7175
 CDS
144..6857
 1..143
 Query Match
Best Local Similarity
Matches 201; Conserv
 5'UTR
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2928 GAGCGGGAGCCCCGACGCGCGCGCGCACCGGCACCGGGATCCGAGCAAGGAGTGCGCC 2987
 2988 GECECCAAGGECEAGGEGEGEGEGEGACCGCCGCGCCCCCGAGGGGGCCCCCGGAG 3047
 3048 eccesaracceses de desecces de consecuences de consecuencias de consec
 3108 caccadectreregaseas de des concesas de des concesas de conces
 610 GGGCAGGCCGGGTGGGAGCAGCACCACCACCGGAGCACCGGAACAGTGTGGCGGCGAT 668
 APPLICANT: Harpold, Michael
APPLICANT: Blis, Steven
APPLICANT: Blis, Steven
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
APPLICANT: Gillespie, Alison
APPLICANT: Gillespie, Alison
APPLICANT: Bredmen, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: METHODS
UNDER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
 CURRANES PATENT PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,272 FILING DATE: US/08/450,272 FILING DATE: US/08/44,950 PRIOR APPLICATION NUMBER: 08/404,950 PRIOR APPLICATION NUMBER: 08/336,257 PRIOR APPLICATION NUMBER: 08/336,257 PRIOR APPLICATION NUMBER: 08/336,257 PRIOR APPLICATION NUMBER: 08/314,083 PRIOR APPLICATION NUMBER: 08/314,083 PRIOR APPLICATION DATE: 28-SEPT-1994 PRIOR APPLICATION DATE: 28-SEPT-1994 PRIOR APPLICATION DATE: 08/311,363 FILING DATE: 23-SEPT-1994 PRIOR APPLICATION NUMBER: 08/311,363 PRIOR APPLICATION NUMBER: 08/311,363 PRIOR APPLICATION DATA: 08/290,012 APPLICATION DATA: 08/290,012
 FILING DAID.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
 UMBER: 08/193,078
07-FEB-1994
 Sequence 8, Application US/08450272
Patent No. 6387696
GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
 1660 Union Street
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 FILING DATE: 07-FEB-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
 San Diego
California
 92101
 COUNTRY:
 STREET:
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 2811 cech-eccachecaneganegecececacedesce--eccesanegececeneseseseseseseseseseses
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCCTCGGTGCTGCTGTTCACTCGGGCGC 309
 310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
 370 CCCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
 3108 CACGAGGCTGTGGAGAAGAGAGACCACGGAGAAGGCCACGGAGAAGAGAGGTGAGAT 3166
 GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Standerman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HETHODS
TITLE OF INVENTION: METHODS
 NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 33,779
REPERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELEPHONE: (619) 450-8400
TELEPHONE: (619) 450-8400
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 Score 49; DB 3; Length 7175;
Pred. No. 0.0091;
0; Mismatches 215; Indels
 CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US

CONTRY: US
 COMPUTER: IBM COMPACTION
COMPUTER: IBM COMPACTION
SOFTWARE: FASESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
 Sequence 8, Application US/08984709A
Patent No. 6320032
 3.8%;
 MOLECULE TYPE: DNA (genomic)
 ATTORNEY/AGENT INFORMATION:
 Query Match
Best Local Similarity 48.0
Matches 201; Conservative
 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 3'UTR
6855..7175
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Eh
 CDS
144..6857
 5'UTR
1..143
 FEATURE:
NAME/KEY:
LOCATION:
 ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-984-709A-8
 FEATURE:
NAME/KEY:
LOCATION:
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1928 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAGGAGTGCGCC 2987
 2988 GGGGCCAAGGGCGAGCGGCGCGCGCACCGCGGCGGCCCCCGAGCGGGGGCCCCGGGAG 3047
 3048 decisionade de de desercados de desercados de contrados de contra
 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGTTCACTCGCGGCGC 309
 310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA: 07/914,231
FILING DATE: 13-JULY-1992
CLASSIFICATION DATA: 07/868,354
FILING DATE: 10-APR-1992
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION HARDER: 07/745,206
FILING DATE: 14-AUG-1991
CLASSIFICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION NUMBER: 33,779
REPERRENCE/DOCKET NUMBER: 33,779
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TELECOMMUNICATION: NUMBER: 33,779
 6362-519812
 TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
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MOLECULE TYPE: DNA (genomic)
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NAME/KEY:
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PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1277
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| ֡          |                                                                                                                                                                                                                                                                      |                                                                           |                                                              |                                                                                                         |                                                                                                         |
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| US-09-844- | σ                                                                                                                                                                                                                                                                    |                                                                           | 7.7                                                          | 98.8                                                                                                    | . 10                                                                                                    |
|            | 18                                                                                                                                                                                                                                                                   |                                                                           | 10.5                                                         | 134.6                                                                                                   | σı                                                                                                      |
| _          | עכ                                                                                                                                                                                                                                                                   |                                                                           | 20.4                                                         | 260.6                                                                                                   | 20                                                                                                      |
|            |                                                                                                                                                                                                                                                                      |                                                                           |                                                              |                                                                                                         | •                                                                                                       |
| US-09-844- | Φ                                                                                                                                                                                                                                                                    |                                                                           | 21.4                                                         | 273.6                                                                                                   | 7                                                                                                       |
| US-09-844- | σ                                                                                                                                                                                                                                                                    |                                                                           | 58.9                                                         | 752.2                                                                                                   | φ                                                                                                       |
| US-10-475  | 18                                                                                                                                                                                                                                                                   |                                                                           | 59.0                                                         | 753.8                                                                                                   | ស                                                                                                       |
| US-10-475  | 18                                                                                                                                                                                                                                                                   |                                                                           | 62.6                                                         | 799.4                                                                                                   | 4                                                                                                       |
| US-09-844- | σ                                                                                                                                                                                                                                                                    |                                                                           | 62.6                                                         | 799.4                                                                                                   | m                                                                                                       |
| US-10-475  | 18                                                                                                                                                                                                                                                                   |                                                                           | 96.6                                                         | 1234.2                                                                                                  | 7                                                                                                       |
| US-09-844- | თ                                                                                                                                                                                                                                                                    |                                                                           | 100.0                                                        | 1277                                                                                                    | ٦                                                                                                       |
|            | 8                                                                                                                                                                                                                                                                    | Length                                                                    | Match                                                        | Score                                                                                                   | No.                                                                                                     |
|            |                                                                                                                                                                                                                                                                      |                                                                           | Ouery                                                        |                                                                                                         | Result                                                                                                  |
|            |                                                                                                                                                                                                                                                                      |                                                                           | dР                                                           |                                                                                                         |                                                                                                         |
| SUMMARI    |                                                                                                                                                                                                                                                                      |                                                                           |                                                              |                                                                                                         |                                                                                                         |
|            | ID<br>US-09-844-864-1<br>US-09-844-864-1<br>US-09-844-864-18<br>US-09-844-864-18<br>US-10-475-502-11<br>US-10-475-502-12<br>US-09-844-864-22<br>US-09-844-864-22<br>US-09-844-864-23<br>US-09-844-864-23<br>US-09-844-864-23<br>US-09-844-864-23<br>US-09-844-864-23 | 1                                                                         | 1                                                            | Query Match Length DB 100.0 1277 96.6 814 9 62.6 6873 18 59.0 4090 18 58.9 9 21.4 305 9 10.5 2074 375 9 | Query Match Length DB 100.0 1277 96.6 814 9 62.6 6873 18 59.0 4090 18 58.9 9 21.4 305 9 10.5 2074 375 9 |

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DB 9; Length 1277; 0; Indels

100.0%; Score 1277; 100.0%; Pred. No. 0; tive 0; Mismatches

Query Match Best Local Similarity 100. Matches 1277; Conservative

; TYPE: DNA ; ORGANISM: Mus musculus US-09-844-864-1

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61 61

1 AAGGCGGGCGAGGCGCGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCG 1 AAGGCGGGCGAGGCGCACCCATGTTCCCGGCGAGCACGTTCCACCCTGCCCG

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|                | 13            | 70.4                        | 5.<br>5    | 105                         | σ       | 9-844-86                                | Sequence 24, Appl  |
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| υ              | ۳             | 51.6                        | 0          | 59816                       | 16      | 80                                      | Sequence 2, Appli  |
|                | 4             | 51                          | ٥.         | 1185                        | 15      | US-10-156-761-6879                      | Sequence 6879, Ap  |
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|                |               | 4 9                         | α          | 6792                        | -       | 115-10-627-370-1                        | Segrence 1. Appli  |
|                | ١ .           | 0                           | . a        | 27.17                       | "       | TIG-10-375-73                           | Semience 13 April  |
|                | ۰,            | 7 4                         | α          | 7177                        | 2 ~     | TR-10-3/3-635 13                        | Semience 7 Appli   |
|                | 4 (           |                             | . 0        | 1111                        | 9 0     | 236-267                                 | Tradity // Sources |
|                | 4 0           | n c                         | . 0        | 1171                        | י ה     | - 726 - 967 -                           | Sequence 33, Appr  |
|                | , ·           | n (                         | 9          | 7007                        | 9 9     | -10-3/5-233-11                          | Sequence II, Appr  |
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|                |               |                             |            |                             |         | ALIGNMENTS                              |                    |
|                |               |                             |            |                             |         |                                         |                    |
| RESULT         | LT 1          |                             |            |                             |         |                                         |                    |
| us-o           | US-09-844-864 | -864-1                      |            |                             |         |                                         |                    |
| ; Se           | quence        | Sequence 1, Application US/ | licat      | ion US/                     | 0984486 | 4864                                    |                    |
| ; Pa           | tent N        | No. US20                    | 02004      | 2926A1                      |         |                                         |                    |
| GE .           | NERAL         | GENERAL INFORMATION         | ATION:     |                             |         |                                         |                    |
| . A            | PPLICA        | Σ                           | zuk,       | Martin                      |         |                                         |                    |
| A              | PPLICA        |                             | an, Yo     | Ren, Yongsheng              |         |                                         |                    |
| Æ .,           | APPLICANT:    |                             | Wu, Xuemei | mei                         |         |                                         |                    |
| H<br>          | TITE C        | TITLE OF INVENTION: OVARY   | TION:      |                             | SPEC    | ENES AND PR                             |                    |
| ·.             | ILE RE        | SPERENCE                    | 3: P01     | FILE REFERENCE: P01925US2 / | 60/     | `                                       |                    |
| ٠.             | URRENT        | r APPLIC                    | 'ATION     | z                           | : ns    | /09/844,864                             |                    |
| ٠.             | CURRENT       | r FILING DATE:              | DATE       | 2001                        | -04-    | 2001-04-27                              |                    |
| <u>а</u>       | RIOR A        | PRIOR APPLICATION NUMBER:   | NOI!       | UMBER: (                    | 60/106  | 06,020                                  | •                  |
| <u>а</u><br>., | PRIOR F       | FILING I                    | ATE:       | FILING DATE: 1998-10-28     | -28     |                                         |                    |
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99.9%;
 Best Local Similarity 99.9
Matches 800; Conservative
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 Sequence 18, Application US/09844864

Patent No. US20020042926A1

JGENERAL INFORMATION

APPLICANT: Matzuk, Martin

APPLICANT: Ren, Yongsheng

APPLICANT: Wu, Kuemei

TITLE OF INVENTION: VOMBR: US/09/844,864

CURRENT FLING DATE: 1098-10-28

PRIOR APPLICATION NUMBER: ECT/US/99/25209

PRIOR APPLICATION NUMBER: ECT/US/99/25209

PRIOR APPLICATION NUMBER: PCT/US/99/25209

PRIOR APPLICATION NUMBER: 1999-10-28

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 18

LENGTH 814
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CONCANISM: mus musculus
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US-09-844-864-18
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Length 814;
 Indels
 Sequence 11, Application US/10475502
Publication No. US20040254132A1
GENERAL INFORMATION:
APPLICANT: Wung, Pei
APPLICANT: Wu, Xuemei
APPLICANT: Bai, Yuchen
APPLICANT: Bai, Yuchen
TITLE OF INVENTION: Ovary-Specific Genes and Proteins
FILE REFERENCE: P01925US7
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Score 799.4; DB 9;
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 GGCTGCAGGGCAGGCGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGC
 GGCGATGCAGTCTGAGCCTGGGAGCGAGGCCATGTCCTGCCGCAGAGATGGCTCAGGA
 3 GGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA
 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGGAGGTTCGGAGCCAAGGGCTGCCG
 CAGCCGTGACGCTGCGGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACT
 CGGGCGCCGCACCTGCAGCCTGCAGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTC
 CTGTCAACCCCGTGGCCACGCCGGCGCGGGAGATCCCCGGCGATCCTGGCAGACCGTAGC
 CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
 Gaps
 ö
 Length 6873;
 Indels
 DB 18;
 Score 799.4; DB 18
Pred. No. 7.4e-227;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/475,502
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: PCT US/2/13245
PRIOR PILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 09/844,864
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3:1
LENGTH: 6873
 GGAGCGCCTGCGTTTCCAGGT 3313
 GGAGCGCCTGCGTTTCCAGTT 803
 Query Match
Best Local Similarity 99.9%;
Matches 800; Conservative
 TYPE: DNA
CORGANISM: mus musculus
US-10-475-502-11
 123
 303
 363
 423
 2993
 3053
 603
 3113
 3173
 3233
 3293
 63
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 GAGAGAGGTGGCCGCGAGGGGTCCCCCCAGCCGCGAAGCGAGGGGGGGAATGTTCA
 602

 122
 120
 182
 242
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 300
 362
 360
 422
 482
 cccerrcrcercerakcerreraradecercrerecreereakagenrecagakacka 480
 542
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 9
 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCTCGAGGGCTGCCG
 GCAGACACCCACGAAGGGAGGAGGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCC
 1 GCCGGCGAGGCGCGGGACGCACCCATGTTCCCCGCCGAGCACGTTCCACCCCTGCCCGCA
 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGGCCAGGGGCTGCCG
 CAGCCACCAGCGGGCACAGCTCATGGCCCTGCTGTCGCGATGGGTCCCCGGTCAG
 CAGCCGTGACGCTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACT
 CGGGCCGCCACGCTGCAGGGTGCCGAGCCAGCCCCGACGCCCCGATCGGGTTC
 CTGTCAACCCCGTGGCCACGCCGCCGCGGAATCCCCGCGATCCTGGCAGACCGTAGC
 CCCGTTCTCGTCGTGACCTTCTGTGGCCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
 3 GGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA
 123 ACCCGCGCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
 Gaps
 13;
 59.0%; Score 753.8; DB 18; Length
97.5%; Pred. No. 2.3e-213;
tive 0; Mismatches 7; Indels
 APPLICANT: Wang, Pei
APPLICANT: Wu, Xuemei
APPLICANT: Wu, Xuemei
APPLICANT: Bai, Yuchen
TITLE OF INVENTION: OVAITY-Specific Genes and Proteins
TITLE OF INVENTION: OVAITY-Specific Genes and Proteins
TITLE OF INVENTION: OVAITY-Specific Genes and Proteins
TITLE OF INVENTION: OVAITY-Specific Genes and Proteins
CURRENT APPLICATION NUMBER: US/10/475,502
CURRENT FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
 i LOCATION: (1)...(4090)
j OTHER INFORMATION: N equals unknown
US-10-475-502-12
; Sequence 12, Application US/10475502
; Publication No. US20040254132A1
; GENERAL INFORMATION:
 Query Match 59.0
Best Local Similarity 97.5
Matches 781; Conservative
 TYPE: DNA ORGANISM: Mus musculus
 NAME/KEY: misc feature
```

us-09-830-810a-1.rnpb

| Db   361 CTGTCAACCCGTGGCCACGCGGGGAGATCCCCGCGATCCTGGCAGACCGTAGC 420  | Qy         603 GGCTGCAGGCCAGCCAGCAGCCACCACCAGGAACCGGAACAGTGTGGC 662 | 723 CCCGGTGATTCGGATGCCCCTCGAGACCAGGCTCCCGGAAAGCACGGAGCAGACAA                                                                                                                                                                                                                                                                    | RESULT 7 US-09-844-864-21 Sequence 21, Application US/09844864 ; Sequence 21, Application US/09844864 ; Patent No. US20020042926A1 ; GENERAL INFORMATION: ; APPLICANT: Martin ; APPLICANT: Ren, Yongsheng ; APPLICANT: Wu, Xuemei ; TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS ; FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48 ; CURRENT APPLICATION NUMBER: US/09/844,864 | CURRENT FILING DATE: 2001-04-27                                                                                                                                                                                                                                                                                   | Query Match 21.4%; Score 273.6; DB 9; Length 305; Best Local Similarity 95.3%; Pred. No. 7.8e-71; Matches 282; Conservative 0; Mismatches 14; Indels 0; Gaps 0; | Oy 965 TGTCAAAGTTGTAAAAGAACTAGATGTGCCTGCCAGTCAGATTTCGCCACGTGGACCT 1024                                                                                                     | OY 1025 AAACGCCCCATCGGCAAAACTTGTGGGAAATGCAAAGAAAACGCCTGTCCTGCGAC 1084                                                           | OY 1085 AGCACCTTCAAGTTCAATACATCATTTAGTGAGAGACGTTTCTGCTAGATGGG 1144                                                                                    | Qy 1145 GCTAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTTTCCAAATTCTT 1204     |
|---------------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|
| Db   541 GAGAGGCCGTGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGCGACGTTCA   600 | Qy 783 GGAGCGCCTGCGTTTCCAGTT 803                                    | Sequence 22, Application US/09844864  PRETENT NO. US2020042926A1  GENERAL INFORMATION:  APPLICANT: Martin  APPLICANT: Ren, Yongeheng  APPLICANT: W. Xuemei  TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS  FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48  CURRENT APPLICANT: NO. NO. NO. NO. NO. NO. NO. NO. NO. NO. | PRIOR APPLICATION NUMBER: 60/106,020                                                                                                                                                                                                                                                                                                                                                     | Query Match         58.9%; Score 752.2; DB 9; Length 809;           Best Local Similarity 97.1%; Pred. No. 3.4e-213;         Indels 5; Gaps 1;           Matches 778; Conservative 0; Mismatches 18; Indels 5; Gaps 1;         I,           Qy         3 GGCGGCGGGGCGCGCACCCATGTTCCCGGCGACGACGTTCCACCCTGCCCGCA 62 | Oy 123 ACCGGGCCCCCTCCTTCCTCCCGGCTACAGACAGCTCATGGCCGGGAGTACGTCGA 182                                                                                             | Qy         183 CAGCCACCAGCGCACACACACACACACACACACACACAGATGGGTCCCGGATGGGTCCCCGGTCAG         242           Db         181 CAGCCACCAGCGGCACAGCTCATGGCCTGCTGCTGTGCGTCCCCGGTCGGT | Qy         243 CAGCCGTGACGCTGCGGTGAACCCGCGCCGCGACGCTCGGTGCAGTGTTCACT         302           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Qy         303 CGGGCGCCGCACGCTGCAGCCTGCCGAGCCCCGAGCCCCGATCGGTTC 362           Db         301 CGGGCGCCGCACGCTGCAGCCTGCAGCCGAGCCCCGAGCCCGGGTCGGGTTC 360 | QY 363 CTGTCAACCCCGTGGCCACGCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGC 422 |

```
; Sequence 23, Application US/09844864
 TYPE: DNA ORGANISM: human
 RESULT 11
US-09-844-864-23
 US-09-844-864-19
 US-09-844-864-19
 US-10-475-502-13
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 986 AGAIGIGCCIGCCCAGICAGAITICGCCACGIGGACCCTAAACGCCCCCATCGGCAAGAC 1045
 1105
 1106 ATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGA 1165
 220
 280
 190 GCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCCCTTTCCCAATTCTT 249
 1205 CATGACAGACAGIGITACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 1260
 101 AGATGTGCCTGCCCAGTCAGACCTCGCCACGTGTACCTTAGACGCCCCCCATCAGCAGAC
 1046 TIGIGIGGAGAIGCAAGGACAAACGCCIGICCIGCGACAGCACCTICAGCITCAAAIAC
 161 ricrereadadarecaadeacaaacecerereceacaecaecereagerreaarae
 250 CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 305
 Gaps
 ;
0
 Length 375;
 Indels
 Sequence 25, Application US/09844864

Patent No. US20020042926A1

Patent No. US20020042926A1

GENERAL INFORMATION:

APPLICANT: Matzuk, Martin

APPLICANT: Matzuk, Martin

APPLICANT: Wu, Xuemei

TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS

FILE REFERENCE: P01925USZ / 09807797 / OTA 99-48

CURRENT APPLICATION NUMBER: US/09/844,864

CURRENT APPLICATION NUMBER: 60/106,020

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.0

SEQ ID NO 25

LINGTH: 375
 Sequence 13, Application US/10475502

Publication No. US20040254132A1

GENERAL INFORMATION:

APPLICANT: Wang, Pei

APPLICANT: Wang, Ratin M.

APPLICANT: Matzuk, Martin M.

APPLICANT: Matzuk, Martin M.

APPLICANT: Pai, Yuchen

TITLE REFERENCE: P01925US;

GURRENT APPLICATION NUMBER: US/10/475,502

CURRENT FILING DATE: 2003-10-22

PRIOR FILING DATE: 2002-04-26

PRIOR APPLICATION NUMBER: US 09/844,864

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-04-27
 DB 9;
 1226 GATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 1260
 GATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 375
 6.3e-67;
 20.4%; Score 260.6;
96.7%; Pred. No. 6.3e
:ive 0; Mismatches
 Best Local Similarity 96.7
Matches 266; Conservative
 TYPE: DNA
CORGANISM: mus musculus
US-09-844-864-25
 RESULT 9
US-10-475-502-13
 US-09-844-864-25
 341
 Query Match
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1480 ACTITICAGCITICAAATACATCATITIAGGIGAAAGICAGTGITIGCIGCGATGCGCTGAIG 1539
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 1420 ceccecececerchaearrierecernearechaaeechaacecererecherekeee 1479
 1540 gagradacgadenteritricogracerecerecerecerecerecerecereres
 1028 CGCCCCCATCGGCAAGACTTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGC 1087
 854
 9
 1088 ACCTICAGCTICAAATACATCATTTA-GTGAGAGTCGAAAACGTTTCTGCTAGATGGGGC
 795 TITCCAGITCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAAATCCGGTG
 9 retreastretrasascasastascascractaretrates assets and a retrease a retrea
 968 CAAAGTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAA
 1147 TAATGGAATGGACAAGTGAGCTTTCTCCCCTTTCACCTCTTCCCTTTCCAAATTCTTCA
 Gaps
 1600 rgaaaggcagrgrarrcrg----aaaagccrrcaaaraaaggrarrgcaa 1646
 1207 TGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAA 1257
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 2
 DB 18; Length 2075;
 Indels
 79; Indels
 Length
 855 GGAGAGCGCCTATGTGTGTGTGTGCAGGCCACCAGTAAGGT 896
 GGAGAGCGCCTATGTGTGGTGTGCAGGGCACCAGTAAGGT 110
 APPLICANT: Martin
APPLICANT: May Xuamei
APPLICANT: Ren, Yongaheng
APPLICANT: Ren, Yongaheng
APPLICANT: Ren, Yongaheng
APPLICANT: Ren, Yongaheng
TITLE CO INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REPERBUCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 1998-10-427
FRIOR PILING DATE: 1998-10-28
FRIOR PILING DATE: 1998-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
SOFTWARE: PATENTIN NUMBER: PCT/US99/25209
STOLING DATE: 1999-10-38
SOFTWARE: PATENTIN VETBION 3.0
 Score 98.8; DB 9;
Pred. No. 6.1e-19;
0; Mismatches 2;
 Score 134.6; DB 1
Pred. No. 4.4e-29;
0; Mismatches 79
 ; Sequence 19, Application US/09844864; Patent No. US20020042926A1; GENERAL INFORMATION:
 7.7%;
 10.5%;
71.1%;
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 2075
 Query Match
Best Local Similarity 71.1;
Matches 207; Conservative
 Conservative
 TYPE: DNA ORGANISM: mus musculus
 Query Match
Best Local Similarity
Matches 100; Conserv
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 795 TITCCAGITCITAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAAICCGGTG 854
 9 TGTTCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGCTGCAAAATCCGGTG 68
 Gaps
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 7.7%; Score 98.8; DB 9; Length 123; 98.0%; Pred. No. 6.1e-19; tive 0; Mismatches 2; Indels
 Length 105;
 0; Indels
 Sequence 20, Application US/09844864
Fatent No. US20020042926A1
GENERAL INPORMATION:
APPLICANT: Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925USZ / 09807797 / OTA 99-48
CURRENT FILING DATE: 2001-04-27
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 25
LENGTH 105
 GENERAL INFORMATION:
APPLICANT: Matzin,
APPLICANT: Matzin,
APPLICANT: Ren, Yongsheng
APPLICANT: Ren, Vongsheng
APPLICANT: Ren, Vongsheng
APPLICANT: Wesmei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REPERENCE: P019250125, / 0980/1844,864
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 1090-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3:0
FROOR DO 23
 69 GGAGAGCGCCTATGTGTGGTGTGTGTGCAGGCACCAGTAAGGT 110
 855 GGAGAGCGCCTATGTGTGTGTGTGCAGGCACCAGTAAGGT 896
 1 Similarity 100.0%; Score 72; DB 9; Le Similarity 100.0%; Pred. No. 5.5e-11; 72; Conservative 0; Mismatches 0;
 Best Local Similarity 98.0
Matches 100; Conservative
 959 ATCACCIGICAA 970
US20020042926A1
 TYPE: DNA
ORGANISM: mus musculus
US-09-844-864-20
 ORGANISM: mus musculus
 72;
 US-09-844-864-20
 US-09-844-864-23
 Query Match
Best Local S:
Matches 72
 TYPE: DNA
 Query Match
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US-09-844-864-24

RESULT 13

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Sequence 8597, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Thou, Yihua
APPLICANT: Baukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Li, Pang
APPLICANT: Selection NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NOS: 204966
 899 TACTICAAACAGTICTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGAC 958
 149 GCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGGGGGCACAGCTCATGG 208
 19 TACTICAAACAGTICTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGAC
 7; Gaps
 ö
 4.3%; Score 55.2; DB 17; Length 1041;
46.2%; Pred. No. 1.4e-05;
tive 0; Mismatches 293; Indels 7;
 5.5%; Score 70.4; DB 9; Length 105; 98.6%; Pred. No. 1.6e-10; Live 0; Mismatches 1; Indels (
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matzuk, Nomei
TITLEO PINVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925USZ / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 1908-10-28
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
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FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
FRIOR APPLICATION NUMBER: PCT/US99/25209
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_15091C.1
US-10-437-963-8597
 Query Match
Best Local Similarity 46.2%
Matches 258; Conservative
 959 ATCACCTGTCAA 970
 Best Local Similarity 98.6
Matches 71; Conservative
 79 GTCACCTGTCAA 90
 TYPE: DNA
CRGANISM: mus musculus
US-09-844-864-24
 TYPE: DNA
ORGANISM: Oryza sativa
 US-10-437-963-8597/c
 Query Match
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RESULT 15
US-10-425-115-17653/C
US-10-425-115-17653/C
Sequence 17653, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBUCE: 38-21(5322)B
CURRENT PILING DATE: 2003-04-28
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 17633
LENGTH: 972
 3;
 ACCCGCGCGCGCGACG----CCTCGGTGCAGTGTTCACTCGGCGCGCCGCACGCTGCAGC 322
 404 cacacadroacida de acacaca canada de acacada de acac
 383 CCGGCGCCGGGAGATCCCCGGCGATCCTGGCAGACCGTAGCCCCGTTCTCGTCGTCGTGACCT 442
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 CTGCAGGGTGCCGAGCCCCGACGCCCGATCGGGTTCCTGTCAACCCCGTGGCCACG 382
CCCTGCTGTCGCGGATGGGTCCCCCGGTCGGTCAGCAGCCGTGACGCTGCGGGTGCAGGTGA 268
 cceseccescicacias de casas de
 21 GGCACCCATGTTCCGGGGGGGGGGGTTCCACCCCTGCCCGCATCCTTATCCGCAGGCCAC
 CAAAGCCGGGGATGGCTGGAGGTTCGGAGGCAGGGGTGCCGACCCGGGCCCCCTTT
 4; Gaps
 Length 972;
 Query Match 4.3%; Score 55; DB 18; Length 97 Best Local Similarity 46.6%; Pred. No. 1.6e-05; Matches 269; Conservative 0; Mismatches 304; Indels
 ; OTHER INFORMATION: Clone ID: MRT4577_116102C.1
US-10-425-115-17653
 LOCATION: (1)..(972)
OTHER INFORMATION: unsure at all n locations
FEATURE:
 GGGAGCAGCAGCACCAC 640
 eccedecececececece 27
 ORGANISM: Zea mays
 NAME/KEY: unsure
 819
 81
 209
 464
 269
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 GGGAGAGGCCCGGCATCCTCGGGACCCGGGAACCGGAGCCGAAGGTGGCCGC 557
141 CCTCCCCGGCTACAGACAGCTCATGGCCGCGGGAGTACGTCG--ACAGCCACCAGCGGGCA 198
 258
 580
 317
 GCAGCCTGCAGGCCGAGCCGCCCGACGCCCGATCGGGTTCCTGTCAACCCCGTGG 377
 460
 579 decelecciones de de
 GTGCAGGTGAAC-CCGCGCGCGCGACGCCTCGGTGTGTTCACTCGGGCGCCCGCACGCT
 | descecedes de contra de
 CAGCTCATGGCCCTGCTGCTGCGGATGGGTCCCGGGTCAGCAGCCGTGACGCTGCG
 244
 GAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGGC 594
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Search completed: January 5, 2005, 21:16:57 Job time: 756 secs